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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: July 7, 2003, 15:47:40; Search time 109 Seconds
(without alignments)
5122.203 Million cell updates/sec

Title: US-09-824-647-16
Sequence: 1 cgcaggcagaccatqtggac.....ataaagtttgtcactttctt 2095
Scoring table: OLIGO
Xgapop 60.0, Xgapext 60.0
Ygapop 6.0, Ygapext 60.0
Fgapop 6.0, Ygapext 60.0
Fgapop 6.0, Pgapext 7.0
Pelop 6.0, Delext 7.0

Total number of hits satisfying chosen parameters: Minlmum DB seq length: 0
Maximum DB seq length: 2000000000

908470 seqs, 133250620 residues

Word size:

Searched:

1687582

Post-processing: Listing first 45 summaries

Command line parameters:
-MODEL-frame+n2p, model -DEV=x1p
-0-/cgn2_1JUSPTO_spool/USO9924647/runat_07072003_154717_26015/app_query.fasta_1.2247
-0-/cgn2_1JUSPTO_spool/USO9924647/runat_07072003_154717_26015/app_query.fasta_1.2247
-DB=A_Geneseq_101002_OFWT-fastan -SUFFIX=std.rag -MINMATCH-0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-blts -STAFT=1 -END=1 -MATRIX=ollgo -TRANS-human40.cd1
-LIST=45 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=45 -MODE-LOCAL
-OUTFWT-pto -NORM-ext -HEAPSIZE=500 -MINLEN-0 -MAXLEN-200000000
-GSER-USO984647_4CGN 1_1.149_erunat_07072003_154717_26015 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -DSPBLOCK=100 -LONGLOG
-NS_TIMPOUT=120 -WARN_TIMEOUT=30 -THRANS_1 -XGAPOP=60 -XGAPOF=60 -FGAPOP=6
-FGAPOP=60 -YGAPOF=60 -DELOP=6 -DELEXT=7
-Database : A_Geneseq_101002:*

A. Ceneseq_101002: *

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2. \\$IDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT: *

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29. \\$IDS2/gcgdata/geneseqq/geneseqp-embl/AA1999.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:

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г	score	Match	Length	9	ar.	neset therein
	593	85.4	593	20	AAW85475	Human GP88 autocri
7	538	. 77.5	593	14	AAR48673	Granulin sequence
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4	410	6	621		AAB43971	
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10	52	7	55	Н	AAR41882	Ö.
11	24	7	54			Granulin C. Homo
c 12	46	•	48	7	AAM59509	Œ
13	34		.56		AAR41885	E
14	32	•	54		AAR41887	C
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16	32		57		ABB07324	receptor
17	32	•	28		ABB07325	receptor
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19	32		65,7		ABB07326	Insulin receptor-I
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27	11	7	25	7	AAR41883	ranuli
28	16		30		AAU82636	Human granulin A-c
29	16		30		AAU82638 .	
30	16	٠	179		AAR15426	
31	15	•	15		AAR35077	N-terminal amino
32	14	٠	14		AAW85481	Human GP88 autocri
33	Ι:	•	15		AAR20737	BGP N-terminal Ir
34	11	•	15		AAR51665	Basophil granule
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	ω (٠	09		364	Human musculoskele
c 41	80		64		254	onibact
42	ω (•	84		370	naman
43	80	•	83		445	novel
77	α	1.2	95	22	~ •	
45	∞	٠	96		AAU14219	Human novel prot

Human GP88 autocrine growth factor.
GP88; granulin; epithilin; human; growth factor; autocrine; tumour; cancer; viral infection; antagonist; therapy; diagnosis.

Homo sapiens.

Key Location/Qualifiers
Peptide 340..364
/note= "E19V peptide used to raise antibody"
Peptide 566..579

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                                                                                                                                                                                                                                           This is the amino acid sequence of human GPBB, an BB kDa glycoprotein autocrine growth factor and epithilin/granulin precursor that is expressed in a tightly requisted manner in normal cells, is overexpressed and unrequisted in highly tumorigenic cells. Glaved from normal cells, and which acts as a stringently required growth simulator for the tumorigenic cells. Inhibition of GPBB expression or action in the tumorigenic cells. Inhibition of GPBB combibilition of the tumorigenic properties of the overproducing inhibition of the tumorigenic properties of the overproducing cells. Antagonists to GPBB are used to treat diseases associated with increased expression of GPBB, particularly cancer but also viral infections. Fragments of GPBB are used to raise specific continuously toxins or other compounds to GPBB-expressing cells) and to screen for antibodies. Wethods are provided for diagnosting cells) and assets or determining susceptibility to disease, resulting from
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treating cancer and viral diseases
from altered GP88 expression
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                     WO9852607-A1
                                         26-NOV-1998
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SHORT ALLES

Alignment Scores: Pred. No.: Sas.00 Matches: Score: Score: Percent Similarity:	Oy 13 ATGTGGACCCTGGTGGCTGGCTTAACAGCAGGCTGGTGGCTGGAACGCGGTGC 72	13 2	0y 193 TGCCAGGTTGATGCCACTGCTGCGGCCACTCTGTTACCGTCTCAGGGACT 252	CGGGGCTTCCACTGCAGAGGGGGGATCCTGCTTCAAAGATCAGGTAACAACTCC 3 CHIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy 373 GTGGGTGCCAGTGCCCTGATAGTCAGTTCGAATGCCCGGACTTCTCCACGTGCTGT 432	Qy 433 GTTATGGTCGATGGCTCCTGGGGGTGCTGCCCCATGCCCCCAGGCTTCCTGTGAAGAC 492	OY 493 AGGGRCCACTGTCCGCACGGTGCCTTCTGCGACCTGGTTCACACCCGCTGCATCACA 552	181 ProfhrGlyThrHillIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Db 201 AlaLeuSerSerValMetCysProAspAlaArgSerArgCysProAspGLySerfnr 220 Qy 673 TGCTGTGGGGTGCCCAGTGGGAAGTATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGC	733	CICLCAMSANAMAN CANCONCALCA CANTANAMAN CONTROLL CONTROLL CONTROLL CANTANAMAN C	3 GATGTGAAATGTGACGAGGTGAGCTGCCCAGATGGCTATACCTGCTGCTGCTACAG 91 	Qy 913 TCGGGGCCTGGGGCTGCTGCTTTACCCCAGGCTGTGTGCTGTGAGGACCACATACAC 972
. 1	Seraldeinfromiainirheeldalaangselfromisvalelyvaleysaspaleid TGTGGGGAAGGACATCTGCCATGATAACCAGACCTGCTGCCGAGACAACCGACAGGGC 	1633 TGGGCCTGCTGCCCTACGCCCAGGGCGTCTGTGTGCTGATCGGCGCCCACTGCTGTCCT 16	501 AladıyPneArgCysAlaArgArgdığılyrini.LysCysLeUArgArgdıArlarry 1753 GACGCCCTTTGAGGGACCCAGCCTTGAGACAGCTGCTG 1791 	xe00/3 AAR48673; AAR48673;	Granulin sequence.	granului, Actalinoyles; wound mealiny, granulocytes; leucocytes. Homo sapiens.	AX FAY Location/Qualifiers FT Misc-difference 452 / Note= "Valine encoded by ATG." FT Misc-difference 539 / Note= "Civolan ancoded by CAG."	WO9315195-A.	28-FEB-1992; 92WO-CA00089. 03-FEB-1992; 92US-0829233. (SOLO/) SOLOMON S.	XX XX DR WPI; 1993-320328/40. DR N-PSDB; AAQ49052.	XX PT New cystine rich granulin peptide(s) from leucocyte(s) - are PT keratinocyte inhibitors useful topically for wound healing XX	Disclosure; Figure 4c; 53pp; English. XX CC The granulin inhibits keratinocytes and is useful in formulations CC for promoting the healing of wounds.	nbəs

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                                         CAGGIGCCCTGGATGGAGAAGGCCCCAGCTCACCTCAGCCTGCCAGACCCACAAGCCTTG
                                                                    AAGAGAGATGTCCCCTGTGATAATGTCAGCAGCTGTCCCTCCTCCGATACCTGCTGCCGA
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                                                                                                                                                                                                                                                                                                                                                        TGTGGGGAAGGACACTTCTGCCATGATAACCAGACCTGCTGCCGAGACAACCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human granulin/epithelin precursor (GP88) protein
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Misc-difference
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human. The method comprises obtaining a biological sample containing chuman. The method comprises obtaining a biological sample containing cells from the patient, detecting GPBB in the cells of the sample, and determining the number of GPBB positive cells in the sample, and determining the ratio of GPBB positive cells in the sample of cells in the sample. The invention also relates to a method for determining if a human patient his resistant to the antineoplastic effects of antioestrogen therapy. The method is useful for diagnosing tumouring antioestrogen therapy. The method is useful for diagnosing tumouring antioestrogen therapy. The method is useful for diagnosing tumouring antioestrogen therapy. The method is useful for diagnosing tumouring antioestrogen therapy. The method is useful for diagnosing tumouring antioestrogen therapy. The method is useful for diagnosing tumouring contains a sample cancer. The method can be used to treat or prevent re-occurrence of cancer in a patient, by administering tamoxifen if the sample contains less than 10 % GPBB, or less than 5 % GPBB positive contains. The present sequence is human granulin/epithelin precursor (GPBB)
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Query Match:
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	1573 TGTGGGGAAGGACACTTCTGCCATGATAACCAGACCTGCCGAGACAACCACAGGGC 	1633 TGGGCCTGCTGTCCCTAGGCCGCTGTTGTTGCTGATCGGCGCCACTGCTGTCCTTCTTTGTTTTTTTT	GCTGGCTTCCGCTGCGCACGCGGGGTACCAAGTGTTTGC 	Qy 1753 GACGCCCTTTGAGGGACCCAGCTTGAGACACTGCTG 1791 	RESULT 4 AAB43971 ID AB43971 standard; Protein; 621 AA.	08-FEB-2001		KW antiluflammatory; antilucit; antilucitic; antibacterial; autilutic; autilutic; autilutic; autilutic; KW antiluflammatory; antiluthyroid; antibacterial; cardiant; KW dermatological; neuroprotective; thrombolytic; coagulant; nootropic; wasotropic; antipsorlatic; antilangiogenic; gene therapy; inflammation;		AX OS Homo sapiens. XX W020055350-A1.	XX XX PD 21-SEP-2000. XX XX XX PF 08-MAR-2000; 2000WO-US05882.	XX	XX			CC in AAB43398 to AAB44239. The proteins can have activities based on the CC tissues and cells the genes are expressed in. Example of activities CC include: cytostatic; proliferative; vulnerary; immunomodulator; CC antidiabetic; antiasthmatic; antirheumatic; antiarthritic;		
	493 AGGGTGCACTGTCGCACGGTGCCTTCTGCGACCTGGTTCACACCCGGTGCATCACA 552 	553 CCCACGGGCACCCCCCTGGCAAAGAAGCTCCCTGCCCAGAGGACTAACAGGGCAGTG 612 	613 GCCTTGTCCAGCTCGGTCATGTGCCGGACGCACGGTCCCGGTGCCTGATGGTTCTACC 672 	673 TGCTGTGGCTGCCCAGTGGGAAGTATGGCTGCTGCCCAATGCCCAACGCCACCTGCTGC 732	733 TCCGATCACCTGCACTGCTGCCCCAAGACACTGTGTGTGACTGATCCAGAGTAAGTGC 792 	793 CTCTCCAAGGAGAACGCTACCACGGACCTCCTCACTAAGCTGCGCACACAGTGGGC 852 	853 GATGTGAAATGTGACATGGAGGTGAGCTGCCCAGATGGCTATACCTGCTGCTGTACAG 912 	913 TCGGGGGCCTGGGCTGCCCTTTTACCCAGGCTGTGTGTGT	973 IGCTGTCCCGGGGGTTTACGTGTGACACGCAGAAGGTACCTGTGAACAGGGCCCCAC 1032 	1033 CAGGGCCCTGGATGGAGAGCCCCAGCTACCAGCCTGCCAGACCCACAAGCCTTG 1092 	1093 AAGAGAGATGTCCCCTGTGATAATGTCAGCAGCTGTCCCTCCC	1153 CTCACGTCTGGGGGTGGGGCTGCTGCTCCAGAGGCTGTCTGCTGCTGGGACCAC 1212 	1213 CAGCACTGCTGCCCCCAGCGATACACGTGTGTAGCTGAGGGGGCAGTGTCAGCGAGGAAGC 1272 	1273 GAGAICGIGGCIGGACIGGAGAAGAIGCCIGCCGCGCGGTICCTIAICCCACCCCAGA 1332 	1333 GACATCGGCTGTGACCAGCACCACCGGGGGGGGGGAACCTGCTGCCGAGCCAG 1392 	1393	1453 TGCTGCCGGCTGGCTACACCTGCAACGTGAAGGCTCGATCCTGCGAAAGAAA	1513 TCTGCCCAGCCTGCCACCTTCCTGGCCCGTAGCCCTCACGTGGGTGTGAAGGACGTGGAG 1572
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or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoletic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and anscersial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 to AAC78457 and AAB44240 represent sequences used in the exemplification of
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Query Match:
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1020 1080 1140 1200 364 960 384 324 344 404 424 GACCÁCATACACTGCTGTCCCGCGGGTTTACGTGTGACACGCAGAAGGGTACCTGTGAA ACCTGCTGCCAACTCACGTCTGGGGAGTGGGGCTGCTGTCCAATCCCAGAGGCTGTCTGC CAGGGGCCCCACCAGGTGCCCTGGATGGAGAAGGCCCCCAGCTCACCTCAGCCTGCCAGAC CCACAAGCCTTGAAGAGAGATGTCCCCTGTGATAATGTCAGCAGCTGTCCCTCCTCCGAT CACACAGIGGGCGAIGIGAAAIGIGACAIGGAGGIGAGCIGCCCAGAIGGCIAIACCIGC ET; growth regulation; inhibition; stimulation TGCTCGGACCACCAGCACTGCTGCCCCCAG 1230 53 53 53 53 53 23 55 page page page page page 'note- "claim 2, page page Location/Qualifiers note-206..262 /label- EP-2 Z 1..593 /label= precursor EP claim 4, 'note- "claim 1, , æ 'n é, AAR14326 standard; Protein; 593 519..574 /label= EP /note= "claim 8 "claim /label EP label= EP note= "claim 282..337 /label- EP-1 ΕP (first entry) Human epithelin precursor 24..180 .497 64..418 'labellabel-'note= Homo sapiens 17-JAN-1992 305 901 325 345 1021 365 1081 385 1141 405 1201 84:1 196 425 AAR14326; Key Protein Protein Protein Peptide Peptide eptide eptide Peptide AAR14326 RÈSULT g à 셤 ŏ 셤 셤 ŏ 셤 ò g å g οğ 셤 ò

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181. AspValLysCysAspMetGluValSerCysProAspGlyTyrThrCysCysArgLeuGln 300
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                                                                                                                                                                                                                                                                                                              TGCTGTCCCGCGCGCGTTTACGTGTGACACGCAGAAGGGTACCTGTGAACAGGGGCCCCAC
                                                                                                                                                                                                                                                                                                                                                                 CTCACGTCTGGGGGGGGGGCTGCTGTCCCAGAGGCTGTCTGCTGCTCGGACCAC
                                                                                        CyscysGluLeuProSerGlyLySTyrGlyCysCysProMetProAsnAlaThrCysCys
                                                                                                                                                                                                                        TGCTGTGAGCTGCCCAGTGGGAAGTATGGCTGCTGCCCAATGCCCAACGCCACCTGCTGC
                                                                                                                                                                              TCCGATCACCTGCACTGCCCCCCAAGACACTGTGTGTGACCTGATCCAGAGTAAGTGC
     AGGGTGCACTGCTGTCCGCACGGTGCCTTCTGCGACCTGGTTCACACCCGCTGCATCACA
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                                                                                                                                                                                                                                   ET-1 is a bifunctional growth regulator, capable of stimulating the growth of some cell types while inhibiting the growth of others. ET-2 is functionally similar to ET-1 w.r.t. growth inhibitory bioactivity. In contrast, however, ET-2 is apparently not capable of eliciting the growth stimulatory activity characteristic of ET-1 and, in fact, antagonises this ET-1 activity. See also AAQ14338-40, AAQ14952-53, AAR14328-9 and AAR15315-20.
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                                                                                                                                                                       - useful
                                                                                                                                                                    New cysteine-rich growth modulating proteins, epithelins - us as inhibitors of neoplastic cell growth and to promote wound healing and treat psoriasis
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                Disclosure; Fig 22; 97pp; English.
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100.00%
100.00%
58.50%
                                                             910S-0083796
900S-0504508
                                         91WO-US02321
                                                                                             (BRIM ) BRISTOL-MYERS SQUIB
                                                                                                                  Plowman GD;
                                                                                                                                       WPI; 1991-325168/44.
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Best Local Similarity:
                                                                                                                                                 N-PSDB; AAQ14339.
                                                                                                                                                                                                                                                                                                                           593
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                                         03-APR-1991;
                                                              13-MAR-1991;
                                                                         03-APR-1990;
WO9115510-A
                    17-0CT-1991
                                                                                                                  Shoyab M,
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21-SEP-2000;
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04-OCT-2000;
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                                                                                                                                                                                                                                                          RESULT 7
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                                                                                                                                                                                                                                                                                                                                                             The present invention describes primer sets for synthesising 5602 (ull-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises at least 15 nucleotides and the combination of the 5'-end sequence. 3'-end sequence; where the oligonucleotide which comprises at least 15 nucleotides and the combination of the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers are also useful for the full-length cDNAs asily without any specialised methods. AAH03629 and AAH03631 to AAH13632 represent human amino acid sequences; and AAH13632 to AAH13632 represent human amino acid sequences; and AAH13632 to AAH13632 represent human amino acid sequences; and AAH13632 to AAH13632 represent human amino acid sequences; and AAH13632 to AAH13632 represent human amino acid sequences; and AAH13632 to AAH13632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       826 ACTAAGCTGCCTGCGCACACAGTGGGCGATGTGAAATGTGACATGGAGGTGAGCTGCCCCA
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                                                                                                                                                                                                                         Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                                                                                                                 Yamamoto J;
                                                                                                                                               Saito K, Yr
, Otsuki T;
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1155
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                               Hayashi K, S
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-824-647-16 (1-2095) x AAB94550 (1-413)
                                                                                                                                                                  Wakamatsu
                                                                                                                                           sogai T, Nishikawa T,
Sugiyama T, Wakamatsu
                 99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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                                                                                                            (HELI-) HELIX RES INST.
                                                                                                                                                                                                  WPI; 2001-318749/34.
                                                                                                                                               Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
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               27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
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29-JUL-1999;
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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention.
                                            1066 CTCAGCCTGCCCACACACACACATGAAGAGATGTCCCCTGTGATAATGTCAGCAGC 1125
152 LysGlyThrCysGluGlnGlyProHisGlnValProTrpMetGluLysAlaProAlaHis 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human brain expressed single exon probe encoded protein SEQ ID NO: 31613.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Single exon nucleic acid probes for analyzing gene expression in human brains -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; brain expressed exon; gene expression analysis; probe; microarray; Alzhelmer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4; SEQ ID NO: 31613; 650pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                 AAM59508 standard; Protein; 77 AA.
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2000US-0234687
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2000GB-0024263
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Best Local Similarity:
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WPI; 2002-083093/11.

The present invention relates to a phage display library of variable heavy domain (VHH or VH) fragments (adab fragments) derived from liama antibodies. The library is useful for in vitro selection against any antibodies. The library is useful for in vitro selection against any antigen of interest as a target. Single domain anti-idiotypic antibody fragments are isolated from the library using phage display technology and an antibody serving as an antigen. Such anti-idiotypic antibody fragments have great potential in evoking the immune system response to pathological antigens and in vaccine development. The large size of the library considerably increases the probability of isolating from it antigen-blinding fragments having high affinity to almost any predetermined target (antigen of interest). The library eliminates the development of anti-idiotypic antibodies by immunisation and allows isolation of anti-idiotypic antibodies. Anu82636-AAM82640 represent peptides used in panning experiments in the present invention. New phage display library of variable heavy domain antigen-binding fragments derived from llama antibodies, useful for in vitro selection against any antigen of interest as a target Disclosure; Page 20; 46pp; English.

30 AA; Sequence

00000 Length: Matches: Conservative: Mismatches: Indels: Gaps: 4.49e-06 16.00 100.00% 100.00% 2.31% 23 Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: Pred. No.:

US-09-824-647-16 (1-2095) x AAU82636 (1-30)

853 GATGTGAAATGTGACATGGAGGTGAGCTGCCCAGATGGCTATACCTGC 900 RESULT

AAU82638;

AAU82638 standard; peptide; 30 AA.

AAU82638

23-APR-2002 (first entry)

Human granulin-A derived peptide substituted version p1781.

Human; phage display library; variable heavy domain fragment; VHH; VH; sdab fragment; single domain anti-idiotypic antibody fragment; phage display technology; immune system response; CDRI/HI; CDR2; CDR3; complementarity determining region; granulin-A; p1781.

Homo sapiens

Synthetic.

WO200190190-A2.

29-NOV-2001.

26-MAY-2000; 2000US-207234P.

25-MAY-2001; 2001WO-CA00763.

CANA) NAT RES COUNCIL CANADA.

Panha J, Dubuc G, Narang S;

WPI; 2002-083093/11.

New phage display library of variable heavy domain antigen-binding fragments derived from llama antibodies, useful for in vitro selection

The present invention relates to a phage display library of variable heavy domain (VHH or VH) fragments (sdab fragments) derived from llama antibodies: The library is useful for in vitro selection against any antibodies: The library is useful for in vitro selection against any antibodies: The library is useful for in vitro selection against any fragments are isolated from the library using phage display technology and an antibody serving as an antigen. Such anti-idiotypic antibody fragments havy great potential in evoking the immune system response to pathological antigens and in vaccine development. The large size of the library considerably increases the probability of isolating from it predetermined target (antigen of interest). The library eliminates the development of anti-idiotypic antibodies by immunisation and allows isolation of anti-idiotypic antibodies. ANUB2636-AAU82640 represent properties and in panning experiments in the present invention. against any antigen of interest as a target Disclosure; Page 20; 46pp; English

Sequence

0000 Conservative: Mismatches: Indels: Matches: 74.49e-06 16.00 100.008 100.008 2.318 Best Local Similarity: Percent Similarity: Alignment Scores: Query Match:

US-09-824-647-16 (1-2095) x AAU82638 (1-30)

853 GATGTGAAATGTGACATGGAGGTGACTGCCCAGATGGCTATACCTGC

RESULT 30

AAR15426 standard; Protein; 179 AA.

AAR15426;

17-JAN-1992 (first entry)

Bovine epithelin precursor (partial).

ET; growth regulation; inhibition; stimulation

Bos taurus.

WO9115510-A.

17-0CT-1991

91WO-US02321 03-APR-1991;

910S-0083796. 900S-0504508. 13-MAR-1991; 03-APR-1990;

(BRIM) BRISTOL-MYERS SQUIB.

Shoyab M, Plowman GD;

WPI; 1991-325168/44. N-PSDB; AAQ14952.

epithelins - useful New cysteine-rich growth modulating proteins, epithelins · us as inhibitors of neoplastic cell growth and to promote wound healing and treat psoriasis

Disclosure; Fig 24; 97pp; English.

The epithelins appear to comprise several distinct members sharing significant structural homology. Two members of the epithelin family,

Matches:

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Score:
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                                                                                                                                                              EP-1 and EP-2, have been purified from natural sources, and cDNAs encoding these and several other members of the epithelin family have been isolated from rat (AAQ14338), human (AAQ14339), bovine, murine (AAQ14340) and chicken (AAQ14953).

ET-1 is a bifunctional growth regulator, capable of stimulating the growth of some cell types while inhibiting the growth of others.

ET-2 is functionally similar to ET-1 w.r.t. growth inhibitory bloactivity. In contrast, however, ET-2 is apparently not capable of eliciting the growth stimulatory activity characteristic of ET-1 and, in fact, antagonises this ET-1 activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid sequence of purified bovine TGFe indicated no homology to other known growth factors. However the N-terminal sequence exhibits considerable amino acid sequence identity to the deduced N-terminal amino acid sequence of human granulin A and the N-terminus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transforming growth factor E produced in commercial quantities -
used for wound healing and burns treatment, comprises monomeric
protein which acts as mitogen for fibroblasts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The partial
                                                                                                                                                                                                                                                                      892 TATACCTGCTGCCGTCTACAGTCGGGGGCCTGGGGCTGCTGCTTTT 939
                                                                                                                                                                                                                                                                                           81
                                                                                                                                                                                                                                                                                Transforming frowth factor e; cell proliferation; mitogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGFe is a glycoprotein with an Mr of about 25,000.
                                                                                                                                                                                                                                                                                                                                                                                                      N-terminal amino acid sequence of human granulin A.
                                                                                                                                                                   Length:
Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                      . AAR35077 standard; protein; 15 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Halper J, Mcgraw RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1993-134386/16.
                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                    Sequence 179 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of epithelin 1.
                                                                                                                                                        Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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Pred. No.:
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This is the amino acid sequence of peptide A14R, comprising amino acid residues A566-R579 of human GP88 (see AAM85475). GP88 is an 88 kba glycoprotein autocrine growth factor that is expressed in a tightly regulated manner in normal cells, is overexpressed and unregulated in highly tumorigenic cells derived from normal cells, and which acts as a stringently required growth stimulator for the tumorigenic cells. A14R was used in an attempt to raise neutralising antibodies to GP88 (see also AAM85480). Antagonists to GP88, such as anti-GP88 antibodies, are used to treat diseases associated with increased expression of GP88, particularly cancer but also viral infections. Anti-GP88 antibodies can also be used a diagnostic reagents and to deliver toxins or other compounds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Composition containing antagonist of growth factor GP88 - useful for treating cancer and viral diseases and also for diagnosing disease from altered GP88 expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ranulin; epithilin; human; growth factor; autocrine; tumour; viral infection; antagonist; therapy; diagnosis; antigen;
                                                                                                                                                                         853 GANGIGAAAIGIGACAIGGAGGIGAGCIGCCCAGAIGGCIAIACC 897
                                                                                                                                                                                                                                                                                                                                                                                                                                Human GP88 autocrine growth factor antigenic peptide A14R.
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                                                                                                                                                                                                                                                                                                      AAW85481 standard; Peptide; 14
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97US-0863079.
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GP88; granulin;
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                        Percent Similarity:
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23-MAY-1997;
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Pred. No.:
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Ξi.

AAR20737;

AAR2073 RESULT

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AAR51665 shows an N-terminal sequence of a basophil granule protein. The BGP can be extracted from human basophil granules by treatment at pH 9.0 or greater. This can be used to generate its corresponding nucleic acid an antibodies. Anti-BGPs are useful for the diagnosis of prepathologic conditions as well as chronic and acute diseases, such as parasitic infection and leukaemia, where there is a change in the amount or distribution of BGPs.
                                                                                                                                                                                                                                                                                                                                                                                            New human basophil granule proteins - and related nucleic acid, expression systems, antibodies, etc., for diagnosis and treatment of e.g. inflammation, parasitic infection, leukaemia etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transforming frowth factor e; cell proliferation; mitogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
Mismatches:
                                           Basophil granule protein; N-terminal sequence; BGP specific antibodies; Antibodies; Leukaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Page 34; 55pp; English.
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                                                                                                                                                                                                                                                                         (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                           (MAYO-) MAYO FOUNDATION
                                                                                                                                                                                                                                                                                                                                                             WPI; 1994-118398/14.
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Best Local Similarity:
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            TXXXI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treatments of cytophoresis from which basophils were recovered.
These were used to search for novel basophil granule proteins (BGP).
The proteins were fractioned. Ca. 25 peaks were identified.
Several fractions were pure enough to allow for the determination of a single amino acid sequence. The N-terminal sequences of eight such fractions are represented in AAR20736-42 and AAR22455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          patient with a form of chronic myelogenous leukemia underwent two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New basophil granule proteins obtd. from cytoplasmic granules for diagnosis and treatment of pathologies involving inflammatory and IgE-mediated responses, infection, hypersensitivity and leukaemia(s)
                                    1708 GCACGCAGGGTACCAAGTGTTTGCGCAGGGAGGCCCCGGGC 1749
                                                      Basophil granule protein; chronic myelogenous leukemia
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US-09-824-647-16 (1-2095) x AAW85481 (1-14)
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RESULT 34 **AAR51665**

Query Match: DB:

AAR51665;

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The present invention describes a method for isolating a polynucleotide of interest that is present or is expressed in a genome of a first mycobacterium strain and that is absent or altered in a genome of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis; Mycobacterium bovis; mycobacterium; detection; BAC vector; bacterial artificial chromosome; tuberculosis
                                                                                                                                                Tighe is a glycoprotein with an Mr of about 25,000. The partial amino acid sequence of purified boyine Tighe indicated no homology to other known growth factors. However the N-terminal sequence exhibits considerable amino acid sequence identity to the deduced N-terminal amino acid sequence of human granulin A and the N-terminus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful for
                                                                          Transforming growth factor E produced in commercial quantities used for wound healing and burns treatment, comprises monomeric protein which acts as mitogen for fibroblasts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolation of polynucleotides from mycobacterial genomes, detection of Mycobacteria and for combating tuberculosis
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Matches:
Conservative:
Mismatches:
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      (UYGE-) UNIV GEORGIA RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB81227 standard; Peptide; 29 AA
                               Parnell PG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis,
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9.00
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1.30%
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                                Mcgraw RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-013262/01.
                                                         WPI; 1993-134386/16.
                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                Sequence 14 AA;
                                                                                                                                                                                                                        of epithelin 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-AUG-2002
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                                                                                                                                                                                                                                                                           Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB81227;
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                                   Halper J,
                                                                                                                                                                                                                                                                                                                                           Query Match:
                                                                                                                                                                                                                                                                                         Pred. No.:
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                                                                                                                                                                                                                                                                                                      Score:
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second mycobacterium strain, which is different from the first strain using a bacterial artificial chromosome (BAC) vector. Recombinant BAC vectors, which are preferably immobilised, can be used to detect may be preferrably immobilised, can be used to detect much a probacterial nucleic acids (genomic DNA, cDNA or mRNA) in biological mycobacterial nucleic acids (genomic DNA, cDNA or mRNA) in biological samples. The polynucleotides identified are useful as probes or primers of or detecting a given mycobacterium of interest. By aligning the polynucleotides contained in the recombinant BAC vectors it is possible to physically map a polynucleotide of mycobacterial origin in a polynucleotide of mycobacterial origin in a polynucleotide of mycobacterial origin in a reseful in providing information for combating tuberculosis. It is are useful in providing information for combating tuberculosis. It is possible to compare genomes between different strains or species and their non-pathogenic strains or species counterparts. ABQ63492 to their non-pathogenic strains or species counterparts. ABQ63492 to their map about the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rat; secreted factor polypeptide; cardiac disease; renal disease; kidney; inflammatory disease; congestive heart failure; myocarditis; asthma; dilated congestive cardiomyopathy; angina pectoris; cardiac arrhythmia; myocardial infarction; pulmonary hypertension; arteriosclerosis; stroke; renal infarction; hereditary nephritis; ophrotis; nephrotic syndrome; renal infarction; hereditary nephritis; polyrystic kidney disease; chronic renal failure; renal vein thrombosis; meduilary sponge kidney; pheumatoid arthritis; osteoarthritis; psoriasis; restenosis; graft versus host reaction; Crohn's disease; ulcerative colitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel secreted factor polypeptide useful for treating cardiac diseases such as arteriosclerosis, myocardial infarction, inflammatory diseases such as asthma, stroke, and rheumatoid arthritis and renal diseases
which is different from the first strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rat secreted factor protein encoded by DNA clone P0239_C11.
                                                                                                                                                                                                                                                                                                                                                             0000873
                                                                                                                                                                                                                                                                                                                                                                                 Matches:
Conservative:
Mismatches: Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alzheimer's disease; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU70166 standard; Protein; 46 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-2001; 2001WO-US09555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-2000; 2000US-193548P.
14-MAR-2001; 2001US-0809545.
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100.00%
100.00%
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N-PSDB; AAS94714.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SCIO-) SCIOS INC.
                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                            29 AA;
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                                                                                                                                                                                                                                                                                                              Sequence
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endothelin, bombesin, endocrine, rhodopsin, opsin,

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                                                             The invention relates to rat secreted factor polypeptides and the polynucleotides encoding them. The sequences are useful for treating cardiac, renal or inflammatory diseases. These include cardiac diseases such as congestive heart failure, myocarditis, dilated congestive cardiomyopathy, angina pectoris, myocardial infarction, cardiac arrhythmia, pulmonary hypertension, arteriosclerosis, atherosclerosis an cardiac tumours, renal diseases such as glomerulomephritis, mephrotic syndrome, renal infarction, hereditary nephritis, polycystic kidney disease, chronic renal failure, renal vein thrombosis and medullary sponge kidney and infammatory diseases such as asthma, rheumatorid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G-protein coupled receptor; ligand binding assay; transmembrane domain; schizophrenia; dopamine; cAMP; adenosine; thrombin; adrenergic; opsin; muscarinic acetylcholine; endothelin; bombesin; endocrine; rhodopsin; odorant; cytomegalovirus; serotonergic.
                                                                                                                                                                                                                                                                                             arthritis, osteoarthritis, stroke, psoriasis, restenosis, graft versus host reaction, Crohn's disease, ulcerative colitis and Alzhelmer's disease. Sequences ANT/0146-ANT/0178 represent the secreted factor polypeptides of the invention.

    useful as antipsychotic agent, e.g.

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Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-824-647-16 (1-2095) x AAU70166 (1-46)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            494 CIGICITCACAGCAGGAAGCCIGG 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuSerSerGlnGlnGluAlaTrp 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW03586 standard; peptide; 56 AA
                          Claim 18; Fig 22; 189pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New dopamine receptor peptide for treating schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93US-0118270.
92US-0943236.
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1.16%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-208785/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                 46 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murphy RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW03586;
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odorant, cytomegaloviral and other GPR proteins. The peptides AAM0378-W03651 represent the N-terminal fragments of the above proteins. The receptor proteins were used to design polypeptides, pref. based on the transmembrane domains, for use in G-protein coupled receptor ligand binding assays. The polypeptide fragments retain biological activity such as binding a GPR ligand or modulating GPR ligand binding to a GPR (see AAM02747-W02999 for examples of polypeptide fragments can be used in compositions for treating subjects suffering from a pathology related to a GPR abnormality e.g. a psychotic disorder such as schizophrenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hyperproliferative disorders and autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                980000
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Matches:
Conservative:
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Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human ORFX protein sequence SEQ ID NO:8572.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP04295 standard; Protein; 58 AA.
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29-AUG-2000; 2000US-228716P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   179
8.00
100.00%
100.00%
1.15%
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                   56 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                   Sequence
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06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
08-SEP-2000;
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in the specification). ABN15762 to ABN27252 encode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polynucleotide syndrome associated with ORFX-associated disorder. ORFX polynucleotide sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, osteoarthritis, neurodegenerative disorders, cirrhosis of liver, osteoarthritis, neurodegenerative disorders, clasted to organ transplantation, cardiovascular diseases, disorders mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage diseases, various immune deficiencies and disorders, infertious atthritis, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune inflammatory eve disease. ORFX proteins are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antidercerial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein;
                                                                                                                                                                                                                                                                                                                                                                        N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                              useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytokine damage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human musculoskeletal system related polypeptide SEQ ID NO 1593.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
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100.00%
1.15%
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Best Local Similarity:
Query Match:
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(HUMA-) HUMAN GENOME SCI INC
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20-OCT-2000;
01-NOV-2000;
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Barash SC, Ruben SM; Rosen CA,

WPI; 2001-451937/48. N-PSDB; AAL35228.

Isolated polypeptide for treating, preventing and, or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g. diagnosis

Claim 11; SEQ ID NO 1593; 781pp + Sequence Listing; English.

The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by

Example 1; SEQ ID No 3740; 1069pp; English.

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SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                        (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and
                                                                                                                                                                                                                  and (f) infectious diseases such as viral, bacterial, rungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wlpo.int/pub/published_pct_sequences.
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protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (antibagonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addisease, allergies, autoimmune haemolytic anneania, autoimmune thyroiditis, diabetes mellitus, crohn's glisease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
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Conservative:
Mismatches:
Indels:
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
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100.008
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                      60 AA;
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Claim 20; SEQ ID No 34063; 103pp; English.

polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO Syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.

P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory cample or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by with mile of immunostric and processing and activity of presence, for example, by with mile of immunostric and processing presence. Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder. 0 0 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels: at ftp.wipo.int/pub/published_pct_sequences Gaps: 1317 GGAACCGCGGCGGCCAGCCATCTT 1294 US-09-824-647-16 (1-2095) x AAU42545 (1-64) Novel human diagnostic protein #3695. 43 GlyThralaAlaGlyArgHisLeu 50 ABG03704 standard; Protein; 84 AA. 30-MAR-2001; 2001WO-US08631. 31-MAR-2000; 2000US-0540217; 23-AUG-2000; 2000US-0649167. 176 8.00 100.00\$ 100.00\$ 1.16\$ (first entry) Percent Similarity: Best Local Similarity: Query Match: 64 AA; WO200175067-A2. Homo sapiens. Alignment Scores: 13-FEB-2002 11-OCT-2001. Seguence ABG03704; :: Q RESULT 42 *5555555555555555555555 à qq

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The invention relates to isolated polynuclectide (I) and probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The can generate the complex production of (II). The can discussed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving quantifating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences of the invention.

Sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO cat fip. wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis; tissue regeneration; immune disorder.
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anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
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Mismatches:
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Best Local Similarity:
Query Match:
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Tang YT, Liu C,

useful in of mutations

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity

Tang YT;

Drmanac RT, Liu C, WPI; 2001-639362/73.

N-PSDB; AAS67891

(HYSE-) HYSEQ INC

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17-JAN-2001; 2001WO-US01334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein levels, as tissue markers, and to isolate receptors or ligands. Polypeptides of the invention may also be useful in treating platelet disorders, stem cell disorders, regenerating bone, cartilage, tendon, ligament and/or nerve tissue, wound healing, treating burns, promoting the proliferation, differentiation and survival of stem cells, as a contraceptive, treating osteoporosis and osteoarthritis, aneama, Alzheimer's, Parkinson's and Huntington's diseases, amylotrophic lateral sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
                                                                                                                                                                                                                                                The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as molecular weight markers, food supplements, and in antibody production. The polypeptides are used to identify compounds which bind to the polypeptides. Polynucleotides of the invention are used as probes and primers, for sequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-sense DNA or RNA and in gene therapy. Polypeptides of the invention can be used to target drugs to a tumour, in assays to determine biological activity, to raise antibodies/elicit an immune response, to determine quantitative
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                                                                                                Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fungal infection or from autoimmunity, cancer, allergy, asthma, graft-versus.host disease, eczema, haemophilia, thrombosis, anti-inflammatory diseases, nervous system disorders, and infection. The present sequence represents a protein of the invention.
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Mismatches:
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Matches:
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                                                                                                                                                                                              Example 4; Page 821-822; 894pp; English.
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WPI; 2001-451939/48.
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Score: Pred.

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(ABB1678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis) diabetes mellitus, Crohn's

Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases

The invention relates to novel genes (ABAll004-ABA21534) and proteins

Claim 11; SEQ ID NO 6087; 1701pp + Sequence Listing; English.

(d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal

epilepsy; and (f) infecti and parasitic infections.

disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias;

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Ruben SM;
                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                       Rosen CA, Barash SC,
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N-PSDB; ABA13756.
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immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral; antibacterial; antialtergic; dermatological; haemostatic; antiasthmatic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis; tissue regeneration; immune disorder.
                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          novel protein; Antianaemic; osteopathic; antiinflammatory;
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Matches:
Conservative:
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Indels:
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Query Match:
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Drmanac RT;

HYSE-) HYSEQ INC Tang YT, Liu C,

WPI; 2001-451939/48. N-PSDB; AAS22524 Isolated polypeptides useful for treating anti-inflammatory diseases nervous system disorders, and for regenerating bone and cartilage -

Example 4; Page 572; 894pp; English.

The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as molypeptides are used to identify compounds which bind to the polypeptides. Polynucleotides of the invention are used as probes and primers, for sequencing, for chromosome or gene mapping, in the prolypeptides. Polynucleotides of the invention are used as probes and primers, for sequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-sense bNA or RNA and in gene therapy. Polypeptides of the invention can be used to target drugs to a tumour, in assays to determine biological activity, to raise antibodies/elicit an immune response, to determine quantitative protein levels, as itssue markers, and to isolate receptors or ligands. Polypeptides of the invention may also be useful in treating platelet disorders, stem cell disorders, regenerating bone, cartilage, tendon, ilgieration, differentiation and survival of stem cells, as a contraceptive, treating osteopoxosis and osteoarthritis, anaemia, and contraceptive, treating osteopoxosis and osteoarthritis, anaemia, and the proliferation of Buttington's diseases, and propertion in the proliferation of Buttington's diseases, and propertion in the proliferation. sclerosis, stroke, immune deficiencies resulting from bacterial, viral or graft-versus-host disease, eczema, haemophilla, thrombosis, anti-inflammatory diseases, nervous system disorders, and infection. The present sequence represents a protein of the invention. ungal infection or from autoimmunity, cancer, allergy, asthma,

Length:
Matches:
Conservative:
Mismatches: Gaps: Percent Similarity: Best Local Similarity: Query Match: Alignment Scores: Pred. No.: Score:

US-09-824-647-16 (1-2095) x AAU14219 (1-96)

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7, 2003, 15:55:14 Search completed: July Job time : 140 secs

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Title:

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Sequence 1416, Ap
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Publication No. US20020183270a1
GENERAL INFORMATION:
APPLICANT: SCITCE GIGETTE
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REPERENCE: 29996.488/P001-A
CURRENT APPLICATION NUMBER: DA100/924,647
CURRENT PILING DATE: 2001-04-04
PRIOR FILING DATE: 2001-04-04
PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-17
PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-17
PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-23
PRIOR FILING DATE: PALON NUMBER: EARLIER PILING DATE: 1997-05-23
SOFTWARE: PALON IN VOI. 2.0
SEQ ID NO 17
LENGTH: 593
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9 US-09-874-056-3
9 US-09-874-056-6
9 US-09-874-056-6
9 US-09-874-056-7
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US-10-245-107-48
US-10-245-171-48
US-10-245-771-48
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Mismatches:
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US-09-824-647-2
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US-10-218-160-2
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-WODEL-frame+_n7p model -DEV-xlp

-WODEL-frame+_n7p model -DEV-xlp

-G-Cgnn2_1/USPTO_spool/US09824647/runat_07072003_154720_26102/app_query.fasta_1.2247

-B-Published_Applications_A -QFWT-fastan -SUFFIX-std_rapb -MINMATCH-0.1

-LOOPEXT-0 -LOOPEXT-0 -UNITS-bits -START-1 -RND-1 -MATRIX-ollgo

-LOOPEXT-0 -LOOPEXT-0 -UNITS-bits -START-1 -RND-1 -MATRIX-ollgo

-LIGNAS-human40.cdi -LIST-45 -DOCALIGN-200 -THE_SCORE_aquality -THR_MIN-1

-ALIGNAS-human40.cdi -LIST-45 -DOCALIGN-200 -MINLEN-0

-AAKLEN-2000000000 -USR-GSO9824647_GCGN_1_1_24_Grunat_07072003_154720_26102

-NCFU-6 -ICPU-3 -NO_MAAP -LARGEQUERY -NEG_SCORES-0 -WAIT -DSSPLOCK-100

-LONGLOG -DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOR-60 -XGAPEXT-60

-FGAPOP-6 -FGAPEXT-7 -YGAPOP-60 -YGAPEXT-60 -DELOP-6 -DELOP-6 -DELEXT-7
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Sequence 17, Appl
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6257.407 Million cell updates/sec
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/ggn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
/ggn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
/ggn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
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//ggn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
                                                                                                                              July 7, 2003, 15:49:17; Search time 77 Seconds
                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

    protein search, using frame_plus_n2p model

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US-10-218-509-17
US-10-281-160-17
US-09-813-156-17
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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
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9 Gaps: 0 ATG1-2095) x US-09-824-647-17 (1-593) ATG1GGACCCTGGTGGCTGGTGGCTGTAACAGGGGCTGGTGGCTGGAACGCGGTGC 72	TGCTGCCGTCCCTTCTGGACAAATGGCCCACAACACTGAGCAGCATCTGGGTGGCCCC 192 [TCCAGTTGCTGCCCCTTCCCAGAGGCCGTGGCATGGGGGATGGCCATCACTGCTGCCCA 312	GTGGGTGCCATCCAGTGCCCTGATAGTCGATTGCCGGACTTCTCCAGGTGCTGT 432	AGGGTGCACTGCTGCACGGTGCCTTCTGCGACCTGGTTCACCACCGCTGCATCACA 552	GCCTTGTCGGCTCGGTCGTCCGGACGGTCCCGGTGCCCTGATGGTTCTACC 672	TCCCATCCAGGGGGCCCCCAAGACACTGTGAGCTGATCCAGAGTAAGTGC 792 TCCCATCAGGGTGCTGCCCCCCAAGACACTGTGTGACCTGATCCAGAGTAAGTGC 792 SETASPH19[H	GATGTGAAATGTGACATGGAGGTGAGCTGCCCAGATGGCTATACCTGCTGCCGTCTACAG 912 ASPVALLYSCYSASPMEtGLUVALSErCYSProAspGlyTyrThrCysCysArgLeuGln 300 TGGGGGCCTGGGGCTGCTGTTACCCAGGCTGTGTGTGTGT	TGCTGTCCCGCGGGGTTTACGTGTGACACGCAGAAGGGTACCTGTGAACAGGGGCCCCAC 1032
: -09-824-647 13 1 73 73	133 TGC 11 41 Cys 193 TGC 11	253 TC 11 81 Se 313 CC	373 G 121 V 433 G 141 V	493 A 161 A 153 G 181 P	13 01 73 73		Qy 853 Db 281 Qy 913 Db 301	Oy 973 ' Db 321 O Oy 1033 O

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ment Scores: 0 ° Length:	593.00 Matches: milarity: 100.00% Conservative:	Best Local Similarity: 100.00% Mismatches: 0	Gaps:	US-09-824-647-16 (1-2095) x US-10-218-509-17 (1-593)	Qy 13 ATGTGGACCCTGGTGACCTGGGTGGCTTAACAGCAGGCTGGTGGCTGGACGCGGTGC 72	Db 1 MetTrpThrLeuValSerTrpValAlaLeuThrAlaGlyLeuValAlaGlyThrArgCys 20	73 CCAGATGGTCAGTTCTGCCTGTGGCCTGGACCCCGGGAGGAGCCAGCTACACC	21 ProAspGlyGlnPheCysProValAlaCysCysLeuAspProGlyGlyAlaSerTyrSer	Qy 133 TGCTGCCGTCCCTTCTGGACAAATGGCCCACAACACTGAGCAGCAGCAGTGGGCGCCC 192	** Cjacjast Griotectespijatipriciiiiii iir teuaetalghiatetetyreiyelyrio	OY 155 SOCROSTINGATION CONTROLLED TO THE CONTROL	QY 253 TCCAGTTGCTGCCCTTCCCAGAGGCGGTGGCGATGGCGATGGCCATCACTGCTGCCCA 312	Db 81 SerSerCysCysProPheProGluAlaValAlaCysGlyAspGlyH18H16CysCysPro 100	Oy 313 CGGGGTTCCACTGCAGTGCAGAGATCCTGCTTCCAAAGATCAGGTAACAACTC 372	Db 101 ArgGlyPheHisCysSerAlaAspGlyArgSerCysPheGlnArgSerGlyAsnAsnSer 120	OY 373 GIGGGIGCCATCCAGIGCCCTGAIAGICAGTICGAAIGCCCGGACTTCTCCACGIGCIGT 432	Db 121 ValG1yAla11eGlnCysProAspSerGlnPheGluCysProAspPheSerThrCysCys 140	433 GTTATGGTCGATGGCTCCTGGGGGTGCTGCCCCATGCCCCAGGCTTCCTGCTGTGAGGCCCAGGCTTGTGTTTTTTTT	141 ValMetValAspGlySerTrpGlyCysCysProMetProGlnAlaSerCysGluAsp	Oy 493 AGGTGCACTGCTGCGCACGGTGCTTCTGCGACCTGGTTCACACCCGCTGCTTCACA 552	553 CCCACGGGCACCCACGCCAAGAAGAAGTCCCTGCCAGAGACTAACAGGGACTA	181 ProfhrGlyfhrHisProLeuAlaLysLysFeuProAlaGlnArgThrAsnArgAlaVal		201 AlaLeuSerSerSerValMetCysProAspAlaArgSerArgCysProAspGlySerThr 22	QY 673 TECTGTGAGCTGCCCAGTGGGAAGTATGGCTGCTGCCCAATGCCCAACGCCACCTGCTGC 732	Db 221 CysCysGluLeuProSerGlyLysTyrGlyCysCysProMetProAsnAlaThrCysCys 240	Qy 733 TCCGATCACTGCTGCTGCCCCAAGACACTGTGTGTGTGTG	Db 241 SerAspHisLeuHisCysCysProGlnAspThrValCysAspLeuIleGlnSerLysCys 260	OY 793 CICICCAAGGAGAACGCTACCACGGACCICCICACTAAGCTGCGCACCACACAGGGC 852	Db 261 LeuSerLysGluAsnAlaThrThrAspLeuLeuThrIJFHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	Qy 853 GATGTGAAATGTGACATGGAGTGAGCTGCCCAGATGGCTATACCTGCTGCTACAGG 912 Ph	913 PCCCCCCTPCPCPCPCPTPTPTPTPCCCACTCTACTCTPCPCPCPC	301 SerGlyAlaTrpGlyCysCysProPheThrGlnalaValCysCysGluAspHisIleHis 32

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ON NUMBER: US/10/281,160
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TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND
FILE REFERENCE: 22996.488/FP011-A
CURRENT APPLICATION NUMBER: US/09/813,156
CURRENT FILING DATE: 2001-03-21
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PRIOR FILING DATE: 1997-12-16
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              AND ANTAGONISTS
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              FACTOR
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Matches:
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Mismatches:
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              GROWTH
     TITLE OF INFERIOR GENETE
TITLE OF INVENTION (GENETE
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWT
FILE REFERENCE: 29996.488/P001-A
CURRENT APPLICATION NUMBER: US/09/824,807
CURRENT FILING DATE: 2001-04-04
PRIOR FILING DATE: 1997-12-16
PRIOR FILING DATE: 1997-12-16
PRIOR FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: 93
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Best Local Similarity: 1
Query Match:
DB:
                                                                                                         ; ORGANISM: Human GP88
US-09-824-807-17
GENERAL INFORMATION:
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GBNE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
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PRIOR APPLICATION NUMBER: US/09/864,761
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-05
PRIOR FILING DATE: 2000-03-05
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PLING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
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Mismatches:
Indels:
                                                                                         APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 1416
                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
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                                                   Sequence 1416, Application
Patent No. US20020052308A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-09-925-301-1416
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                                      -09-925-301-1416
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EST_HUMAN HIT: BE742164.1, EVALUE 6.00e-20
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Matches:
                CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-32
PRIOR FILING DATE: 2000-08-03
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-10-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2000-05-21
PRIOR PELING DATE: 2000-09-21
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FILING DATE:\2001-01-30
APPLICATION NUMBER: PCT/USO1/00668
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                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US01/00666 FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01/00667 APPLICATION NUMBER: PCT/US01/00667 APPLICATION NUMBER: PCT/US01/00664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
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OTHER INFORMATION:
OTHER INFORMATION:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
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  CURRENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTGTGTGCTGCGAGGATCGCCAGCACTGCTGCCCGGCTGCTACACCTGCAAGACGTGAAG 1485
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EST_HUMAN HIT: BF344549.1, EVALUE 8.000
SWISSPROT HIT: P28799, EVALUE 8.00e-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 43653 LENGTH: 77
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Matches:
Conservative:
Mismatches:
Indels:
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APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
                                                                                                                                                                                                                                FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PCT/US01/00670 PRIOR FILING DATE: 2001-01-30
                                                      PCT/US01/00669
                                                                                                      APPLICATION NUMBER: PCT/US01/00665
                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US01/00661
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
APPLICATION NUMBER: PCT/US01/00664
                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/234,687 PRIOR FILING DATE: 2000-09-21
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Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: MAP TO AC003043.1 OTHER INFORMATION: EXPRESSED IN BRAI OTHER INFORMATION: EST HUMAN HIT: BF OTHER INFORMATION: SWISSPROT HIT: P2
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                        DATE: 2001-01-30
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
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Best Local Similarity:
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Sequence 7, Application US/09874056

Sequence 7, Application No. US20020192704A1

GENERAL INFORMATION:
APPLICANT: OKANO, Akira
APPLICANT: ETO, Tuzuru
APPLICANT: IZUMI, Tetsuro
TITLE OF INVENTION: Isame
FILE REFERENCE: 209427050
CURRENT FILING DATE: 2001-06-06
PRIOR PLILING DATE: 2001-06-06
PRIOR PLILING DATE: 2000-06-07
PRIOR FILING DATE: 2000-06-07
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1396 GGGAGCTGGCTGCTGCCAGTTGCCCCATGCTGTGTGCTGCGAGGATCGCCAGCACTGC 1455
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                  22 GlySerTrpalaCysCysGlnLeuProHisAlaValCysCysGluAspArgGlnHisCys 41
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Sequence 2, Application US/09824647;
Publication No. US20020183270a1
GENERAL INFORMATION:
FULL OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
TITLE OF INVENTION: 88 KDA TUMORER: US/09/824,647
CURRENT FILING DATE: 20996.488/P001-A
PRIOR APPLICATION NUMBER: US/09/824,647
PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-17
PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATEORIL VOIT 2.0
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Mismatches:
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US-09-824-647-2
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SOFTWARE: PatentIn version 3.1
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US-09-874-056-7
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Best Local Similarity:
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LENGTH: 589
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US-09-874-056-7
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APPLICANT: OKANO, Akira
APPLICANT: OKANO, Akira
APPLICANT: ETO, Yuguru
APPLICANT: ETO, Yuguru
APPLICANT: IZUMI, Tetsuro
TITLE OF INVENTION: Same
TITLE OF INVENTION: Same
TITLE OF INVENTION: Same
CURRENT APPLICATION NUMBER: US/09/874,056
CURRENT APPLICATION NUMBER: US/09/874,056
CURRENT PILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: JP 2000-170912
PRIOR APPLICATION NUMBER: J000-06-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.1
                  Sequence 4, Application US/09874056
Publication No. US20020192704A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ETO, YUZUTU
APPLICANT: IZUMI, Tetsuro
TITLE OF INVENTION: Insulin Receptor-Related Receptor Binding Protein and Utilization
TITLE OF INVENTION: Same
FILE REFERENCE: 209427USO
CURRENT APPLICATION NUMBER: US/09/874,056
CURRENT FILING DATE: 2001-06-06
PRIOR RIPLING DATE: 2000-06-07
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Publication No. US20020192704A1
                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
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Best Local Similarity:
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US-09-874-056-5
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LENGTH: 58
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TYPE: PRT
ORGANISM: *Mouse epithelin/granulin
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US-09-813-156-2
LENGIH: 589
                                 US-10-281-160-2
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Publication No. US20030092661A1
GENERAL INFORMATION:
APPLICATION TO USABATION:
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 2996, 488/P001-A
CURRENT APPLICATION NUMBER: US/10/218,509
CURRENT FILING DATE: 1998-08-15
PRIOR APPLICATION NUMBER: 08/991,862
PRIOR PLING DATE: 1998-08-17
PRIOR PLING DATE: 1998-08-17
PRIOR PLING DATE: 1999-08-17
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Mismatches:
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            Conservative:
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                                                                      US-09-824-647-16 (1-2095) x US-09-824-647-2 (1-589)
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Matches:
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
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SOFTWARE: PatentIn Ver. 2.0
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Best Local Similarity:
                        Best Local Similarity:
Query Match:
DB:
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US-10-281-160-2
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1396 GGGAGCTGGCCTGCTGCCAGTTGCCCCATGCTGTGCTGCGAGGATCGCCAGCACTGC 1455
                                                                                                                                                     479
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GENERAL INFORMATION:

APPLICANT: Serrero, Ginette

TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS

FILLE REFERENCE: 29996.488/P001-A

CURRENT APPLICATION NUMBER: 08/09/813,156

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 08/991,862

PRIOR APPLICATION NUMBER: 08/893,862

PRIOR PILING DATE: 1997-12-16

PRIOR FILING DATE: 1997-05-23

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2

LENGTH: 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 460 GlySerTrpAlaCySCysGlnLeuProHisAlaValCySCySGluAspArgGlnHisCyS
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Patent No. US20020094966A1
GENERAL INFORMATION:
APPLICATE: Seriero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996.488/P001.A
CURRENT APPLICATION NUMBER: US/09/824,807
CURRENT FILING DATE: 2001-04-04
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                     US-09-824-647-16 (1-2095) x US-10-281-160-2 (1-589)
                                                                                         Gaps:
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US-09-813-156-2
                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09813156; Patent No. US20020061859A1
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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Sequence 6, Application US/10218509
; Publication No. US20030092661A1
; GEBREAL INFORMATION:
APPLICANT: Serrero, Ginette
; TITLE REPERENCE: 29996.488/P001-A
; CURRENT APPLICATION NUMBER: 08/510/218,509
; CURRENT FILING DATE: 2002-08-15
; PRIOR PILICATION NUMBER: 08/991,862
; PRIOR PILICATION NUMBER: 08/991,862
; PRIOR PILICATION NUMBER: 08/981,862
; PRIOR PILICATION NUMBER: 08/981,862
; PRIOR FILING DATE: 1998-08-17
; RADOR APPLICATION NUMBER: 08/981,862
; SOFTWARE: PATERIE 1997-05-23
; NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/10281160
; Publication No. US20030108950A1
; GENERAL INFORMATION:
APPLICANT: Serrero, Ginette
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: 29996.4884/P001-A
; CURRENT APPLICATION NUMBER: US/08/291,862
; PRIOR FILING DATE: 1998-08-17
; PRIOR FILING DATE: 1998-08-17
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver: 2.0
; SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: PEPTIDE

LOCATION: (1)...(19)

O'THER INFORMATION: Internal peptide of human GP88 used to develop

CTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody.

US-10-218-509-6
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OTHER INFORMATION: Internal peptide of human GP88 used to develop oTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody
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Matches:
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ORGANISM: Human granulin
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Best Local Similarity:
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Best Local Similarity:
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Pred. No.:
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TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996.488/P001-A
CURRENT APPLICATION NUMBER: US/09/824,647
CURRENT FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/991,862
PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-17
PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 6
LENTH: 19
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OTHER INFORMATION: Internal peptide of human GP88 used to develop
OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody
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    PRIOR APPLICATION NUMBER: 08/991,862
PRIOR FILING DATE: 1997-12-16
PRIOR PRICATION NUMBER: 08/863,862
PRIOR FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 2
LENGTH: 589
                                                                                                                                                                                             ; ORGANISM: Mouse epithelin/granulin US-09-824-807-2
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Publication No. US20020183270A1
GENERAL INFORMATION:
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Query Match:
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Query Match: DB:

RESULT 18 US-10-218-509-6

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; ORGANISM: Mus musculus
US-09-874-056-3
                                                                                                         Percent Similarity:
Best Local Similarity:
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US-09-824-807-6
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| Sequence 6, Application US/09824807
| Sequence 6, Application US/09824807
| Parent No. US202001094966A1
| GENERAL INFORMATION: BETTER OF INVENTION: BRAD TUMORICENIC GROWTH FACTOR AND ANTACONISTS
| TILLE REFERENCE: 29996.484/P001-A
| CURRENT APPLICATION NUMBER: US/09/824,807
| CURRENT FILING DATE: 2001-04-04
| PRIOR PELICATION NUMBER: 08/991,862
| PRIOR FILING DATE: 1997-12-16
| PRIOR FILING DATE: 1997-12-16
| PRIOR FILING DATE: 1997-12-16
| SOFTWARR: PATENTION VOINGER: 108/863,862
                                                                     1048 GAGAAGGCCCCAGCTCCACCTCAGCCTGCCACAAGCCTTGAAGAGAGATGTC 1104
                                                                                                                                                                                               Sequence 6, Application US/09813156
; Sequence 6, Application US/09813156
; Patent No. US20020061859A1
; GENERAL INFORMATION:
APPLICANT: Serrerc, Ginette
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REPERENCE: 29996.4881/P001-A
; CURRENT APPLICATION NUMBER: 08/09/813,156
; CURRENT FILING DATE: 1997-12-16
; PRIOR PLICATION NUMBER: 08/961,862
; PRIOR PLICATION NUMBER: 08/963,862
; PRIOR FILING DATE: 1997-12-16
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PATENTIN VET. 2.0
; SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (1)...(19)
OTHER INFORMATION: Internal peptide of human GP88 used to develop
OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(19)
OTHER INFORMATION: Internal peptide of human GP88 used to develop
OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody
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                         US-09-824-647-16 (1-2095) x US-10-281-160-6 (1-19)
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ORGANISM: Human granulin
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Best Local Similarity:
Query Match:
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Pred. No.:
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Sequence 3, Application US/09874056;
Sequence 3, Application US/09874056;
Publication No. US20020192704A1
GENERAL INFORMATION:
APPLICANT: OKANO, Akira
APPLICANT: ETO, Yukuru
APPLICANT: IZUMI, Tetsuro
TITLE OF INVENTION: Insulin Receptor-Related Receptor Binding Protein and Utilizat
TITLE OF INVENTION: Same
FILE REFERENCE: 2094270S0
CURRENT APPLICATION NUMBER: US/09/874,056
CURRENT PILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: JP 2000-170912
PRIOR APPLICATION NUMBER: JP 2000-170912
PRIOR SEQ ID NOS: 8
SOFTWARE: Patentin Version 3.1
SEQ ID NO 3
SEQ ID NO 3
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Publication No. US20020192704A1
GENERAL INFORMATION:
APPLICANT: CRANO, Akira
APPLICANT: ETO, Yuzuru
APPLICANT: IZUMI, Tetsuro
TITLE OF INVENTION: Insulin Receptor-Related Receptor Binding Protein and Utiliza
TITLE OF INVENTION: Same
FILE REFERENCE: 209427US0
CURRENT APPLICATION NUMBER: US/09/874,056
CURRENT APPLICATION NUMBER: JP 2000-170912
PRIOR FILING DATE: 2000-06-07
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                    Matches:
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SOFTWARE: PatentIn version 3.1
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PatentIn Ver. 2.0
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SOFTWARE:
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Publication No. US20030092661A1
GENERAL INFORMATION:
APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996.488/P001.A
CURRENT APPLICATION NUMBER: US/10/218,509
CURRENT FILING DATE: 2002-08-15
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REPERENCE: 2996.488/P001.A
CURRENT APPLICATION NUMBER: US/09/824,647
CURRENT FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 08/991,862
PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-17
PRIOR PILING DATE: EARLIER RELING DATE: 1998-08-17
PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (1)...(14)
OTHER INFORMATION: Internal peptide of human GP88 used to develop
OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody
                                                                                                                                                                                                                                                      1396 GGGAGCTGGCCTGCTGCCAGTTGCCCCATGCTGTGTGCTGCGAGGAT 1443
                                                                                                                                                                                                                                                                          22 GlySerTrpAlaCysCysGlnLeuProHisAlaValCysCysGluAsp 37
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Mismatches:
Indels:
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                                                                           Length:
Matches:
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PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 08/863,862
PRIOR FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/09824647
Publication No. US20020183270A1
GENERAL INFORMATION:
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14.00
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16.00
100.00%
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 14
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; ORGANISM: Mus musculus
US-09-874-056-6
                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
Query Match:
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US-10-218-509-7
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US-09-824-647-7
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                                                                         Pred. No.:
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Sequence 7, Application US/10281160
Publication No. US20030108950A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 20996.488/P001.A
CURRENT APPLICATION NUMBER: US/10/281,160
CURRENT FILING DATE: 1998-08-17
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1999-05-23
                                                   COCATION: (1)..(14)
CTHER INFORMATION: Internal peptide of human GP88 used to develop
CTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody
US-10-218-509-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (1)..(14)
OTHER INFORMATION: Internal peptide of human GP88 used to develop
OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody
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Mismatches:
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Mismatches:
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Matches:
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Patent No. US20020061859A1
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SOFTWARE: PatentIn Ver. 2.0
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APPLICANT: Serrero, Ginette
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ORGANISM: Human granulin
TYPE: PRT
ORGANISM: Human granulin
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Best Local Similarity:
Query Match:
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Best Local Similarity:
                                               NAME/KEY: PEPTIDE LOCATION: (1)..(14
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US-09-809-545A-43; Sequence 43, Application US/09809545A; Sequence 43, Application US/09809545A; Setence 43, Expert No. US-20020110804A1; GENERAL INFORMATION:
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LOCATION: (19)
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US-09-764-877-1593
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TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS FILE REFERENCE: 2996.488/P001-A CURRENT APPLICATION NUMBER: US/09/813,156 CURRENT APPLICATION NUMBER: 08/991,862 PRIOR APPLICATION NUMBER: 08/991,862 PRIOR PILING DATE: 1997-12-16 PRIOR PILING DATE: 1997-05-23 NUMBER OF SEQ ID NOS: 17 SOFTWARE: PATENT NOS: 17 SOFTWARE: PATENT NET: 1997-05-23 NUMBER OF SEQ ID NOS: 17 SEQ ID NOS: 17 LENGTH: 14
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; CTHER INFORMATION: Internal peptide of human GP88 used to develop
; CTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody
US-09-824-807-7
                                                                                                                                                                                                                                                                                                                                                      LOCATION: (1)..(14)
OTHER INFORMATION: Internal peptide of human GP88 used to develop
OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody
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Mismatches:
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Matches:
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Matches:
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Patent No. US20020094966Al
GENERAL INFORMATION:
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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1708 GCACGCAGGGGTACCAAGTGTTTGCGCAGGGAGGCCCCGCGC 1749

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. OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-877-1593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REPERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
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Mismatches:
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APPLICANT: Stanton, Lawrence W.
APPLICANT: White, R. Tyler
TITLE OF INVENTION: SECRETED FACTORS
FILE REFERENCE: SCIOS.017A
CURRENT APPLICATION NUMBER: US/09/809,545A
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 84
SQUTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 43
LENGTH: 46
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Matches:
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Patent No. US20020147140A1
GENERAL INFORMATION:
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SOFTWARE: Patentin Ver. 2.
SEQ ID NO 1593
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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Sequence 18, Application US/10237271

Sequence 18, Application No. US20030096328A1

SEQUENCE USCAMATION

SEQUENCE USCAMATION

SERVINGANT: THE BURNHAM INSTITUTE

APPLICANT: SMITH, Jeffrey W.

APPLICANT: AXELROD, Funiko T.

TITLE OF INVENTION: SERINE/THREONINE HYDROLASE PROTEINS AND SCREENING ASSAYS

FILE REFERENCE: BUTMAI100-1

CURRENT APPLICATION NUMBER: US/10/237,271

CURRENT APPLICATION NUMBER: US 60/317,842

PRIOR PLILING DATE: 2001-09-06

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Patentin version 3.1

SEQ ID NO 18

TENGTH: 166

TYPE: PRIOR
                                                                                                                               US-09-824-647-16 (1-2095) x US-09-925-301-1558 (1-109)
               Conservative:
Mismatches:
Indels:
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Mismatches:
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Matches:
Matches:
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APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: APO-2 LIGAND
FILE REFERENCE: 11669.220503
CURRENT APPLICATION NUMBER: US/09/934,465
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: 08/584,031
PRIOR FILING DATE: 1996-01-09
NUMBER OF SEQ ID NOS: 17
SOFFWARE: PATENTI VET. 2.0
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LOCATION: (3)..(8)
FOTER INFORMATION: Xaa is any Amino Acid
FEATURE:
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               Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
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No..
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1558, Application US/09925301
Patent No. US20020052308A1
GENERAL INFORMATION:
TELE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT FAPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR PILING DATE: 1909-03-12
PRIOR PILING DATE: 1999-03-12
                                                                                                           APPLICANT: Simmons, Carl.
TITLE OF INVENTION: Malze Proteinase Inhibitor-Like
TITLE OF INVENTION: Malze Proteinase Inhibitor-Like
TITLE OF INVENTION: Polynucleotides and Methods of Use
FILE REFERENCE: 35718/239836 CURRENT APPLICATION NUMBER: US/10/039,836A
CURRENT FILING DATE: 2001-10-23
PRIOR PLILING DATE: 2000-10-25
NUMBER OF SEQ ID NOS: 4
SOFTHARE: PastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 97
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Mismatches:
Indels:
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Matches:
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                                    Sequence 2, Application US/10039836A publication No. US20030033632A1 GENERAL INFORMATION:
APPLICANT: Crane, Virginia
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SOFTWARE: Patentin Ver. 2.
SEQ ID NO 1558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: SITE
LOCATION: (80)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JS-09-925-301-1558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
             US-10-039-836A-2
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NAME/KEY: MISC_FEATURE

109

Length:

223

Alignment Scores:

Pred. No.:

Pred. No.:

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ION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ION: ACIDS ENCODING THE SAME
                           TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME PILE REFERENCE: P3630RJC112
CURRENT APPLICATION NUMBER: US/10/245,103
CURRENT FILING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: 10/197942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-824-647-16 (1-2095) x US-10-245-103-48 (1-192)
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NUMBER OF SEQ ID NOS: 116
SEQ ID NO 48
LENGTH: 192
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                                                                                                                                                                                                                                                                                                                    R FILING DATE: 1998-03-27
R APPLICATION NUMBER: 60/086478
R FILING DATE: 1998-05-22
R APPLICATION NUMBER: 60/08/607
R FILING DATE: 1998-06-02
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Publication No. US20030068779A1
GENERAL INFORMATION:
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Gurney, Austin
Smith, Victoria
                                                                                                                                                                                                                                             FILING DATE: 1997-10-24
APPLICATION NUMBER: 60/065027
FILING DATE: 1997-11-10
APPLICATION NUMBER: 60/079689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/090689
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Watanbe, Colin
                                                                                                                                                                                                                        APPLICATION NUMBER: 60/063046
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/089801
                                                                                                                                                              APPLICATION NUMBER: 60/059114
FILING DATE: 1997-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 1998-06-18
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Best Local Similarity:
Query Match:
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Pred. No.:
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TILLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPERENCE: 29-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: US/201-204089
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR APPLICATION NUMBER: UP 2001-272697
PRIOR APPLICATION NUMBER: UP 2001-272697
                                                                                                                                                                                                   Gaps:
COCATION: (32)..(56)
COTHER INFORMATION: Xaa is any Amino Acid
US-10-237-271-18
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Publication No. US20030068778A1
GENERAL INFORMATION:
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Grimaldi, J. Christopher
Gurney, Austin
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US-10-156-761-12579
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Watanbe, Colin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: OMURA, SATOSHI
APPLICANT: ISHIKDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
                                                                                                                                       100.00%
100.00%
1.15%
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Best Local Similarity:
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Best Local Similarity:
Query Match:
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US-10-156-761-12579
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LENGTH: 190
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Length:
Matches:
Conservative:
Mismatches:
Indels:

Gaps:

- See File Wrapper or PALM

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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3630R1C98
                                       PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR RILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or Palm.
NUMBER OF SEQ.ID NOS: 116
SEQ.ID NO 48
LENGTH: 192
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PRIOR APPLICATION NUMBER: 10/197942
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Publication No. US20030068781A1
GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/063046
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APPLICATION NUMBER: 60/065027
FILING DATE: 1997-11-10
      60/087607
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Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
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APPLICATION NUMBER: 60/087607
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Watanbe, Colin
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Filvaroff, Ellen
                            FILING DATE: 1998-0 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hang,2emin
                                                                                                                                                                                                                                                                           ; ORGANISM: Homo Sapien
US-10-245-143-48
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                                                                                                                                                                                                                                                                                                                                            Alignment Scores
                                                                                                                                                                                                                                                         TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                              Pred. No.:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE GAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative:
Mismatches:
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Matches:
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FILE REFERENCE: PS50RLG90
CURRENT APPLICATION NUMBER: US/10/245,143
CURRENT FILING DATE: 2002-09-16
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NUMBER OF SEQ ID NOS: 116
SEQ ID 448
LENGTH: 192
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R RAPELICATION NUMBER: 60/087607
R PTLING DATE: 1998-06-02
R APPLICATION NUMBER: 60/089801
R FILING DATE: 1998-06-18
R RAPLICATION NUMBER: 60/090557
R R RAPLICATION NUMBER: 60/090557
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Goddard, Audrey
Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
                   60/063046
                                FILING DATE: 1997-10-24
APPLICATION NUMBER: 60/065027
                                                                                                    APPLICATION NUMBER: 60/079689
FILING DATE: 1998-03-27
                                                                                                                                            APPLICATION NUMBER: 60/086478
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PRIOR FILING DATE: 1998-06-25
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Sequence 48, Application US/10245143; Sequence 48, Application US/10245143; Publication No. US20030068780A1; GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
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Watanbe, Colin
                                                                                 FILING DATE: 1997-11-10
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1997-09-17
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  ILING DATE: 1997-0
PPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
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                   PRIOR A
PRIOR A
PRIOR B
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Length:
Matches:
Conservative:
Mismatches:

Indels:

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APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3630981770
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Matches:
Conservative:
Mismatches:
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                                                    Conservative:
Mismatches:
Indels:
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                                    Matches:
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                  ength:
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                                                                                                                 Gaps:
                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
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PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
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RIOR APPLICATION NUMBER: 60/079689
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PRIOR APPLICATION NUMBER: 60/087607
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Grimaldi, J. Christopher
                                                                                                                                                                                                                                                                                             5-10-245-883-48
Sequence 48, Application US/10245883
Publication No. US20030068783A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smith, Victoria
Stephan, Jean-Phillippe
Watanbe, Colin
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PRIOR FILING DATE: 1998-06-18
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SEQ ID NO 48
LENGTH: 192
TYPE: PRT
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Best Local Similarity:
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Query Match:
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US-10-245-883-48
    Alignment Scores:
Pred. No.:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3630R1C93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - See File Wrapper or PALM
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 48
; LEWGTH: 192
; TYPE: PRT
; ORGANISM: Homo Saplen
US-10-245-771-48
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Matches:
Conservative:
Mismatches:
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CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
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Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 48
LENGTH: 192
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PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-10-24
PRIOR PILING DATE: 1997-11-10
PRIOR PILING DATE: 1997-11-10
PRIOR PILING DATE: 1997-11-10
PRIOR FILING DATE: 1998-03-27
PRIOR PLING DATE: 1998-03-27
PRIOR PLING DATE: 1998-03-27
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FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/089801
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Publication No. US20030068782A1
GENERAL INFORMATION:
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Grimaldi, J. Christopher
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Watanbe, Colin
Wood, William
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Smith, Victoria
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CORGANISM: Homo Sapien
US-10-245-851-48
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Best Local Similarity:
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APPLICATION NUMBER: 60/177118
FILING DATE: 2000-01-20
APPLICATION NUMBER: 60/179851
FILING DATE: 2000-02-02
APPLICATION NUMBER: 60/180921
FILING DATE: 2000-02-08
                             CATION NUMBER: 60/138385 IG DATE: 1999-06-09
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FILLING DATE: 1999-07-20
APPLICATION NUMBER: 60/145698
FILING DATE: 1999-07-26
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PPLICATION NUMBER: 60/150114
ILING DATE: 1999-08-20
PPLICATION NUMBER: 60/151700
ILING DATE: 1999-08-31
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PPLICATION NUMBER: 60/141037
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FILING DATE: 1999-07-20
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PPLICATION NUMBER: 60/148188
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PLICATION NUMBER: 60/149395
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FILING DATE: 2000-09-01
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ING DATE: 1999-08-31
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PPLICATION NUMBER: 60/170262
LLING DATE: 1999-12-09
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PPLICATION NUMBER: 60/222695
ILING DATE: 2000-08-02
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ILING DATE: 1999-08-12
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LING DATE: 2000-04-18
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FILING DATE: 2000-09-15
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FILING DATE: 2000-09-22
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FILING DATE: 2000-09-05
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LING DATE: 2000-05-2
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CURRENT FILING DATE: 2002-09-06
794 TCTCCAAGGAGAACGCTACCACGG 817
                       JURGENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: 10/197942
                                                                                                        Application US/10237535
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Grimaldi, J. Christopher
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FILING DATE: 1998-11-03
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APPLICATION NUMBER: 60/119342
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Stephan, Jean-Phillippe
Watanbe, Colin
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                                                                                                             GENERAL INFORMATION:
APPLICANT: Bate. "
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                                                                                                      Sequence 48,
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APPLICATION NUMBER: 60/261910

CATION NUMBER: 10/081056 4G DATE: 2002-02-20 APPLICATION NUMBER: 10/119480 FILING DATE: 2002-04-09 Alignment Scores: Score:

APPLICATION NUMBER: 09/941992

2001-08-28

CATION NUMBER: 10/052586

APPLICATION NUMBER: 10/001054

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: US-09-824-647-16 (1-2095) x US-10-237-535-48 (1-192) Percent Similarity: Best Local Similarity: Query Match:

ITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ITLE OF INVENTION: ACIDS ENCODING THE SAME ILE REFERENCE: P3630R1C11 CURRENT APPLICATION NUMBER: US/10/238,183 CURRENT FILING DATE: 2002-09 PRIOR FILING DATE: 1998-11-03
PRIOR PLING DATE: 1998-11-03
PRIOR PLING DATE: 1999-01-12
PRIOR PLING DATE: 1999-01-12
PRIOR PLING DATE: 1999-02-09
PRIOR PLING DATE: 1999-02-09
PRIOR PLING DATE: 1999-03-12
PRIOR PLING DATE: 1999-03-12
PRIOR PLING DATE: 1999-03-12
PRIOR PLING DATE: 1999-03-11
PRIOR PLING DATE: 1999-03-11
PRIOR PLING DATE: 1999-04-01
PRIOR PLING DATE: 1999-04-01
PRIOR PLING DATE: 1999-04-01
PRIOR PLING DATE: 1999-05-17
PRIOR PLING DATE: 1999-05-17
PRIOR PLING DATE: 1999-05-11 RIOR APPLICATION DATE: 1998-07-04
RIOR FILING DATE: 1998-07-07
RIOR APPLICATION NUMBER: 60/091978 APPLICATION NUMBER: 60/106932 FILING DATE: 1998-11-03 APPLICATION NUMBER: 60/115554 ALPING DATE: 1999-01-12 FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090689
FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/091358 FILING DATE: 1998-07-01 RIOR APPLICATION NUMBER: 60/099803 RIOR APPLICATION NUMBER: 10/197942 APPLICATION NUMBER: 60/087607 APPLICATION NUMBER: 60/089801 APPLICATION NUMBER: 60/090557 RESULT 43
US-10-238-183-48
US-10-238-183-48
; Sequence 48, Application US/10238183
; Publication No. US20030073189A1
; GENERAL INFORMATION: Goddard, Audrey Grimaldi, J. Christopher Gurney, Austin 60/059114 Smith, Victoria Stephan, Jean-Phillippe Watanbe, Colin 1998-09-10 998-06-02 FILING

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APPLICATION NUMBER: 60/150114
FILING DATE: 1999-08-20
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ILING DATE: 2000-01-20
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APPLICATION NUMBER: 60/18/202
APPLICATION NUMBER: 500/18/202
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PLICATION NUMBER: 60/145228
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ING DATE: 1999-12-09
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APPLICATION NUMBER: 60/206330
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APPLICATION NUMBER: 60/222695
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APPLICATION NUMBER: 60/230621
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LICATION NUMBER: 60/140653
ING DATE: 1999-06-22
                                     LICATION NUMBER: 60/141037
ING DATE: 1999-06-23
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FILING DATE: 2000-09-22
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APPLICATION NUMBER: 09/802706 FILING DATE: 2001-03-09 APPLICATION NUMBER: 09/872035 LING DATE: 2001-06-01
PLICATION NUMBER: 09/918585
LING DATE: 2001-07-30 PPLICATION NUMBER: 09/924419 ILING DATE: 2001-08-06 PPLICATION NUMBER: 09/927796 FILING DATE: 2002-02-20 APPLICATION NUMBER: 10/119480 FILING DATE: 2002-04-09 LING DATE: 2001-02-09 PELICATION NUMBER: 60/274399 LING DATE: 1999-11-10 PPLICATION NUMBER: 09/709238 LING DATE: 2000-11-08 APPLICATION NUMBER: 09/929404 FILING DATE: 2001-08-13 APPLICATION NUMBER: 09/941992 FILING DATE: 2001-08-28 APPLICATION NUMBER: 09/946374 PPLICATION NUMBER: 10/001054 ILING DATE: 2001-11:30 FILING DATE: 2001-04-03 APPLICATION NUMBER: 60/282129 PLICATION NUMBER: 10/052586 PLICATION NUMBER: 60/264395 APPLICATION NUMBER: 60/267623 APPLICATION NUMBER: 60/282199 APPLICATION NUMBER: 60/290589 APPLICATION NUMBER: 09/267213 APPLICATION NUMBER: 09/380138 APPLICATION NUMBER: 09/423741 CATION NUMBER: 10/081056 60/266421 APPLICATION NUMBER: 60/280982 PLICATION NUMBER: 09/180997 APPLICATION NUMBER: 09/380137 APPLICATION NUMBER: 09/403297 2001-08-09 2001-02-02 2001-03-09 001-05-09 1998-11-19 LING DATE: 1999-10-18 2001-04-04 -09-04 001-04-04 002-01-1 1999-08-2 1999-03--80-6661 FILING DATE: LING DATE: ILING DATE: LING DATE: LING DATE: LING DATE Alignment Scores: PRIOR PRIOR

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US-09-824-647-16 (1-2095) x US-10-238-183-48 (1-192)

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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
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PRIOR FILLING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
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ORGANISM: Homo Sapien
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CURRENT APPLICATION NUMBER: US/10/238,283
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 10/197942
PRIOR PELLING DATE: 2002-07-18
PRIOR PELLING DATE: 1997-09-17
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Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
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Application US/10238283 to. US20030073190A1
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Watanbe, Colin
Wood, William
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NUMBER OF SEQ ID NOS: 116
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6-phosphofructokin lipopolysaccharide endo-1,4-beta-gluc

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N'Alternate names: epithelin N'Contains: granulin A; granulin B; granulin C; granulin D; granulin E; granulin I C; Species: Homo sapiens (man) C; Date: 30-Sep-1992 #sequence_revision 03-May-1996 #text_change 08-Dec-2000 C; Accession: JC1284; A38128; A38118; A36698; B36698; C36698; D36698; A56873 R; Bhandari, V; Bateman, A. Biochem. Biophys. Res. Commun. 188, 57-63, 1992 A;Title: Structure and chromosomal location of the human granulin gene. A;Reference number: JC1284; MUID:93038704; PMID:1417868 granulin precursor [validated] - human A; Accession: JC1284

A; Molecule type: DNA
A; Residues: 1-593 <BHA>
R; Residues: 1-593 <BHA>
B; Polomann (6.D.; Green, J.M.; Neubauer, M.G.; Buckley, S.D.; McDonald, V.L.; Todan
J. Biol. Chem. 267, 13073-13078, 1992.
A; Title: The epithelin precursor encodes two proteins with opposing activities on
A; Reference number: A38128; MUID:92317004; PMID:1618805

A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-593 <PLO> A; Accession: A38128

A;Cross-references: GB:X62320; NID:g31192; PIDN:CAA44196.1; PID:g31193
R;Bhandari, V.; Palfree, R.G.E.; Bateman, A.
Proc. Natl. Acad. Sci. U.S.A. 89, 1715-1719, 1992
A;Title: Isolation and sequence of the granulin precursor cDNA from human bone man A;Reference number: A38118; MUID:92179253; PMID:1542665
A;Accession: A38118

A; Molecule type: mRNA

A; Residues: 1-406, R', 408-433, G', 435-453, 'G', 455-459, 'Q', 461-546, 'A', 548-566, 'R', A; Cross-references: GB: M75161; NID: 9183612; PIDN: AAA58617.1; PID: 9183613
A; Note: this sequence has been revised in reference JC1284
B; Bateman, A: Belcourt, D:; Bennett, H.; Lazure, C:; Solomon, S.
Biochem. Biophys. Res. Commun. 173, 1161-1168, 1990
A; Title: Granulins, a novel class of peptide from leukocytes.
A; Reference number: A36698; MUID: 91097544; PMID: 2268320

ALIGNMENTS

agaE protein [impo oxidoreductase Atu

NOL1/NOP2/sun

potassium channel

Database

Post-processing: Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	dranulin precursor	epithelin/granulin	epithelin/granulin	acrogranin quine	antimicrobial pept	sensory transduct1	gene u-shaped prot	variant surface ql	hypothetical profe	variant surface ql	hypothetical prote	hypothetical prote		hypothetical prote
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æ	Query Match	58.5	4.6	4.6	3.7	1.3	1.3	1.3	1.2	1.2	1.2	1.2	1.2	1.2	1.2
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NiAlternate names: acrogranin; PC-cell-derived growth factor C;Species: Mus musculus (house mouse) C;Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 20-Aug-1999 C;Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 20-Aug-1999 C;Accession: C38128; S32503; 199468; A46705 Buckley, S.D.; McDonald, V.L.; Todaro J. Biol. Chem. 267, 13073-13078, 1992
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CCCACGGGCACCCACCCCTGGCAAAGAAGCTCCCTGCCCAGAGGACTAACAGGGCAGTG
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A/introns: 46/3; 88/3; 117/1; 154/3; 200/1; 236/3; 279/1; 311/3; 393/3; 471/3; 548/3
A/introns: 46/3; 88/3; 117/1; 154/3; 200/1; 236/3; 279/1; 311/3; 393/3; 471/3; 548/3
C/Superfamily: granulin
C/Superfamily: granulin
C/Superfamily: granulin fattus predicted <AMT>
C/Superfamily: granulin fattus predicted <AMT>
C/Superfamily: granulin fattus predicted <GRP>
C/Superfamily: granulin fattus predicted <GRP>
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C/Superfamily: granulin fattus experimental <GRP>
C/Superfamily: granulin fattus predicted 
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A; Residues: 281-336 cBAT>
A; Note: this protein was purified and characterized as granulin A
A; Accession: B36698
A; Molecule type: protein
A; Residues: 206-218, "H', 220-233 cBAZ>
A; Molecule type: protein
A; Residues: 364-367, "X', 369-385, "H', 387-396 cBA3>
A; Note: this protein was purified and characterized as granulin C
A; Accession: D36698
A; Molecule type: protein
A; Residues: 442-446, "XDTSS', 456-458, "DG' cBA4>
A; Molecule type: protein
A; Residues: 442-446, "MUID: 93229246; PMID: 8471426
A; Accession: A56873; MUID: 93229246; PMID: 8471426
A; Accession: A56873; MUID: 93229246; PMID: 8471426
A; Residues: 281-283, "X', 285-289, 'S', 291-295 cKAR>
A; Experimental source: urine
A; Rosidues: 281-283, "X', 285-289, 'S', 291-295 cKAR>
A; Experimental source: urine
A; Note: sequence extracted from NCBI backbone (NCBIP: 129524)
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Matches:
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Cross-references: GDB:136006; OMIM:138945
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R;Baba, T.; Hoff, H.B. Mol. 1993 Mol. Reprod. Dev. 34, 233-243, 1993 A;Title: Acrogranin, an acrosomal cysteine-rich glycoprotein, is the precusor A;Reference number: 148141; MUID:93228994; PMID:8471244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acrogranin - guinea pig (fragment)
C;Species: cavia porcellus (guinea pig)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999
C;Accession: I48141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1396 GGGAGCTGGGCCTGCTGCCAGTTGCCCCATGCTGTGTGCTGCGAGGATCGCCAGCACTGC
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A; Residues: 279-307, 5B',310-324, 'T',326,'X',328,'Q' < BAT>
A; Residues: 279-307, 5B',310-324,'T',326,'X',328,'Q' < BAT>
B; Bhandari, V.; Glaid, A.; Bateman, A.
B; Bhandari, V.; Glaid, Bateman, A.
B; Endocrinology 133, 2682-2689, 1993
A; Title: The complementary deoxyribonucleic acid sequence, tissue distrib.
A; Reference number: 153272, MUID: 94062640; PMID: 8243292
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-200,'S', 203-388,'M', 390-589 < RES>
A; Cross-references: GB: M97750; NID: 9204223; PIDN: AAA16903.1; PID: 9204224
C; Superfamily: granulin
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C;Superfamily: granulin
                                           R;Bateman, A.; Belcourt, D.; Bennett, H.; Lazure, C.; Solomon, Blochem. Blophys. Res. Commun. 173, 1161-1168, 1990
A;Title: Granulins, a novel class of peptide from leukocytes. A;Reference number: A36698; MUID:91097544; PMID:2268320
A;Accession: E36698
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Mismatches:
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A;Molecule type: mRNA
A;Residues: 1-591 <RES>
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A.Residues: 18-349, L',351-589 <BAB>
A.Residues: 18-349, L',351-589 <BAB>
R.Baba, T.: Hoff, H.B.
A.Ti. Hoff, H.B.
A.Title: Acrogranin, an acrosomal cysteine-rich glycoprotein, is the precusor of the grown and acrosomal cysteine-rich glycoprotein, is the precusor of the grown and acrosomal cysteine-rich glycoprotein, is the precusor of the grown and acrossion: 149468
A.Reference number: 149468
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: mRNA
A.Molecule type
       epithe
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A; Residues: 1-589 <PLO>
A; Residues: 1-580 <PLO>
A; Crossidues: 1-580 <PLO>
A; Crossidues: 1-580 <PLO>
A; Crossidues: 1-580 <PLO
A; Reference number: 322, 89-94, 1993
A; Title: Exon/intron organization of the gene encoding the mouse epithelin/granulin pred
A; Reference number: $32503; MUID: 93245991; PMID: 8482392
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A;Residues: 18-19,'X',21-25,'X',27-29,'XX',32;'XXX',119-127;152-154,'DXK',158-161,'X',16
C;Superfamily: granulin
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Jul-1992 $sequence_revision 10-Jul-1992 $text_change 20-Aug-1999
C;Accession: B38128; A36199; B36199; B36699; B36272
R;Plowman, G.D.; Green, J.M.; Neubauer, M.G.; Buckley, S.D.; McDonald, V.L.; Todaro, G.J.
J. B101. Chem. 267, 13073-13078, 1992
A;Title: The epithelin precursor encodes two proteins with opposing activities on epithe
A;Reference number: A38128; MUID:92317004; PMID:1618805
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A; Residues: 1-589 <PLC>
A; Residues: 1-589 <PLC>
A; Residues: 1-589 <PLC>
A; Cross-references: GB:X62322; NID:g56108; PIDN:CAA44198.1; PID:g56109
A; Cross-references: GB:X62322; NID:g56108; DIDN:CAA44198.1; PID:g56109
B; Shoyab, M.; McDonald, V.L.; Byles, C.; Todaro, G.J.; Plowman, G.D.
Proc. Natl. Acad. Sci. U.S.A. 87, 7912-7916, 1990
A; Title: Epithelins 1 and 2: isolation and characterization of two cysteine-rich growth-A; Reference number: A36199; MUID:91045907; PMID:2236009
A; Rocession: A36199
A; Molecule type: protein
A; Residues: 280-300 <SHO>
A; Molecule type: protein
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A; Cross-references: GB:M86736; NID:g191766; PIDN:AAA37191.1; PID:g191767
R; Zhou, J.; Gao, G.; Crabb, J.W.; Serrero, G.
J. Blol. Chem. 268, 10863-10869, 1993
A; Title: Purification of an autocrine growth factor homologous with mouse epithelin A; Reference number: A46705; MUID:99266526; PMID:8496151
A;Title: The epithelin precursor encodes two proteins with opposing activities on A;Reference number: A38128; MUID:92317004; PMID:1618805
A;Accession: C38128
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Matches:
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Pred. No.:
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RESULT

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A, Description: acts as a transregulator of achaete and scute in the dorsal region of
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C;Species: Salmonella typhimurium
C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 30-Sep-1993
                                                                                                                                                                                                                                    A; Cross-references: EMBL: Y12322; NID: e1169964; PID: e1169965; PIDN: CAA72991.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Trypanosoma equiperdum
C;Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 26-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     variant surface glycoprotein 20 BC1 RF2 - Trypanosoma equiperdum (fragment)
             C;Species: Drosophila melanogaster
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
C;Accession: T13850
                                                                                                                               Si.
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R;Thon, G.; Baltz, T.; Elsen, H.
Renes Dev. 3, 1247-1254, 1989
A;Title: Antigent diversity by the recombination of pseudogenes.
A;Reference number: A32986; MUID:90006746; PMID:2792762
gene u-shaped protein - fruit fly (Drosophila melanogaster)
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Matches:
Conservative:
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Mismatches:
Indels:
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A;Molecule type: mRNA
A;Residues: 1-1191 <HAE>
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Matches:
                                                                                         R; Haenlin, M. submitted to the EMBL Data Library, April 1997 Submitted to the EMBL Data Library, April 1997 A; Accession: T13850
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A; Residues: 1-71 < THO>
A;Cross-references: GB:X17158
C; Superfamily: variant surface glycoprotein
C; Reywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1632 GCCCTGTCGGTTGTCTCGGCAGCA 1609
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R; Finlay, B.B.; Frost, L.S.; Paranchych, W.
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                                                                                                                                                                                                                                                                                                             Cross-references: FlyBase: FBgn0003963
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Query Match:
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Query Match:
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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-633 < MAN>
A; Cross-references: EMBL:D90911; GB:AB001339; NID:g1653083; PIDN:BAA18086.1; PID:d101881
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sensory transduction histidine kinase sll1228 - Synechocystis sp. (strain PCC 6803) N;Alternate names: protein sll1228 C;Species: Synechocystis sp. A;Variety: PCC 6803 A;Variety: PCC 6803 C;Date: 25-Apr-1997 *sequence_revision 25-Apr-1997 *text_change 08-Oct-1999 C;Accession: S75525
      antimicrobial peptide eNAP-1 - horse (fragment)
C;Species: Equus caballus (domestic horse)
C;Accession: A4794; A40833
R;Couto, M.A.; Harwig, S.S.; Cullor, J.S.; Hughes, J.P.; Lehrer, R.I.
Infect Immun. 60, 3065-3017, 1992
A;Rtle: Identification of eNAP-1, an antimicrobial peptide from equine neutrophils.
A;Reference number: A44794; MUID:92347972; PMID:1639474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F.420-531/Domain: response regulator homology <RRH>
F.468/Binding site: phosphate (Asp) (covalent) #status predicted
                                                                                                                                                                                                                                                                        A;Experimental source: neutrophils
A;Note: sequence extracted from NCBI backbone (NCBIP:109730)
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A; Accession: S75525
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Matches:
Conservative:
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Matches:
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Reywords: phosphoprotein
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Query Match:
                                                                                                                                                                                                                                                                                                                        Superfamily: granulin
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Best Local Similarity:
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                                                                                                                                                                                    A; Accession: A44794
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ArItle: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic
A; Reference number: A82950; MUID:20437337; PMID:10984043
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                                                                                                                                                          A; Cross-references: GB:U67586; GB:L77117; NID:g1592096; PIDN:AAB99470.1; PID:g1592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, J.; Loury, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein PA0679 [imported] - Pseudomonas aeruginosa (strain PA01) C;Species: Pseudomonas aeruginosa C;Species: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                          A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-135 <BUL>
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C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15585
                                                                                                                                                                                                                             A;Nap position: FOR1427020-1427427
A;Start codon: GTG
C;Superfamily: Methanococcus jannaschil hypothetical protein MJ1457
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A;Description: The sequence of C. elegans cosmid C24A3
A;Reference number: Z18373
A;Reference number: Z18373
A;Accession: T15585
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Reldues: 1-150 cFRV>
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Matches:
Conservative:
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A,Experimental source: strain PAO1
C,Genetics:
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                      A;Accession: H64481
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A;Gene: PA0679
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Nature 293, 230-233, 1981
Nature 293, 230-233, 1981
A;Title: Two variant surface glycoproteins of Trypanosoma brucei have a conserved C-term A;Reference number: A17609; MUID:82013622; PMID:7278981
A;Accession: S07326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A. Molecule type: mRNA
A. Residues: 1-115 CARTH>
A. Residues: 1-115 CARTH>
A. Residues: 1-115 CARTH>
A. Cross-references: EMBL:J01227; NID:g162397; PIDN:AAA30292.1; PID:g162398
A. Yote: the authors translated the codon GCT for residue 53 as Ser
C. Superfamily: variant surface glycoprotein
C. Keywords: blocked carboxyl end; glycoprotein; lipoprotein; membrane protein; phosphati
F: 1-92/Product: variant surface glycoprotein (clone Angrat 1.8) (fragment) #status predict
F: 93-115/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F: 42/Binding site: carbohydrate (Asn) (covalent) #status predicted
F: 92/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asp) (in mature form)
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R; Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, F. Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, F. Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Fachor, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A; Atthors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C. A; Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschila A; Reference number: A64300; MUID; 96337999; PMID: 8688087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - Trypanosoma brucei (fragment)
J. Bacteriol. 168, 990-998, 1986
A;Title: Nucleotide sequence of the traYALE region from IncFV plasmid pED208.
A;Reference number: A91828; MUID:87056998; PMID:2877970
A;Accession: E2561
A;Accession: E2561
A;Accession: A;Access
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C;Species: Methanococcus jannaschil
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            variant surface glycoprotein AnTat 1.8 precursor - Trypanosoma brucei (fragm
C;Species: Trypanosoma brucei
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 31-Jan-2000
C;Accession: S07326; A17609
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uypornetical protein UL26 - human cytomegalovirus (strain AD169)
C; Species: human cytomegalovirus, human herpesvirus 5
A;Note: host Homo sapiens (man)
C;Date: 07-5ep-1990 #sequence_revision 07-5ep-1990 #text_change 21-Jan-2000
C;Accession: S09789
R;Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, M.; Barrell, B.G.
Curr. Top. Microbiol. Immunol. 154, 125-169, 1990
A;Title: Analysis of the protein-coding content of the sequence of human cytomegalox A;Reference number: S09749; MUID: 90269039; PMID: 2161319
A;Status. .....
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A;Note: this sequence was submitted to the EMBL Data Library, December 1989
C;Superfamily: human cytomegalovirus hypothetical protein UL26
                                                                                                                                                                                                                                                                                                                                                                                       c;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-188 <CHE>
                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: T08793
R; Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann,
Submitted to the Protein Sequence Database, May 1999
A; Reference number: 216468
A; Accession: T08793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-181 <KOE>
A;Cross-references: EMBL:AL050173
A;Experimental source: adult uterus; clone DKF2p586F0422
                                                                                                                                                                                                                                                                                                                                                          hypothetical protein DKFZp586F0422.1 - human (fragment)
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A;Note: DKFZp586F0422.1
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A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
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Experimental source: strain Nigg (MoPn)
    A;Cross-references: EMBL:U40424; NID:91065542; PID:91065544; PIDN:AAA81456.1; CESP:C24A3
C;Genetics:
A;Gene: CESP:C24A3.5
A;Introns: 88/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein CT303 - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C; Species: Chlamydia trachomatis
C; Stock Cession: E71530
R; Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998
A; Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trach, R; Reference number: A71570; MUID:99000809; PMID:9784136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession: E71530
Status: preliminary
Molecule type: DNA
Residues: 1-171 <ARN>
Cross-references: GB:AE001303; GB:AE001273; NID:q3328718; PIDN:AAC67896.1; PID:q332871
Experimental source: serotype D, strain UW-3/Cx
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C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Date: 31-Mar_2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
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A;Gene: CT303
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US-09-824-647-16 (1-2095) x S09789 (1-188)

Aliqument Scores

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A.Map position: 1
C. Superfamily: cytochrome c4; cytochrome c6 homology
C. Superfamily: cytochrome c4; cytochrome c6 homology
C. Keywords: chromoprotein; duplication; electron transfer; heme; iron; metalloprc
C. Keywords: chromoprotein; duplication; electron transfer; heme; iron; metalloprc
F; 51-122/Domain: cytochrome c6 homology <CYCl>
F; 60,63/Binding site: heme (cys) (covalent) % status predicted
F; 64,103/Binding site: heme iron (His, Met) (axial ligands) % status predicted
F; 151,206/Binding site: heme iron (His, Met) (axial ligands) % status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Species: Popilia japonica (Japanese beetle)
C; Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 01-Dec-2000
C; Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 01-Dec-2000
C; Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 01-Dec-2000
C; Date: 22-Sep-1993 #sequence novel.
R; Burke, W.D.; Eickbush, D.G.; Xiong, Y.; Jakubczak, J.; Eickbush, T.H.
Mol. Biol. Evol. 10, 163-185, 1993
A; Title: Sequence relationship of retrotransposable elements R1 and R2 within and A; Reference number: A44490; MUID:93196484; PMID:8383793
A; Accession: F44490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the rRNA genes of
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Mismatches:
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A; Residues: 1-245 <BUR>
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Best Local Similarity:
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A; Residues: 175-191 <
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Query Match:
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                                                                                                                                                                                                                                 Nilternate names: CD27-Ligand; CD27LG
C;Species: Homo saplens (man)
C;Species: Homo saplens (man)
C;Species: Homo saplens (man)
C;Species: Homo saplens (man)
C;Date: 16-Feb-1994 #sequence_revision 23-Aug-1996 #text_change O5-Nov-1999
C;Accession: 1562l4; A40738
N;Bowman, M.R.; Crimmins, M.A.; Yetz-Aldape, J.; Kriz, R.; Kelleher, K.; Herrmann, S.
J. Immunol. 152, 1756-1761, 1994
A;Title: The cloning of CD70 and its identification as the ligand for CD27.
A;Reference number: 1562l4; MUID: 94165470; PMID: 8120384
A;Recession: 1562l4
A;Retus: translated from GB/EMBL/DDBJ
A;Retus: translated from GB/EMBL/DDBJ
A;Retus: translated from GB/EMBL/DDBJ
A;Retus: translated from GB/EMBL/DDBJ
A;Retus: translated from GB/EMBL, TDBJ
A;Reterences: GB:S65339; NID: 941654772; PIDN: AAB30121.1; PID: 9545773
A;Title: Molecular and biological characterization of a ligand for CD27 defines a new fa
A;Retus: Array, Ar
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C.; Ma
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A,Residues: 1-229 <MHI>
A,Cross-references: GB:AE002078; GB:AE000513; NID:g6460306; PIDN:AAF12028.1; PID:g646036
A,Experimental source: strain R1
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T.; Zalewski,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A/Gene: GDB:CD70; CD27LG
A/Coss-references: GDB:139157
A/Cross-references: GDB:139157
A/Cross-references: GDB:139157
C/Map position: 19p13-19p13
C/Map position: 19p13-19p13
C/Map position: 19p13-19p13
C/Map position: Transmembrane #status predicted <TMM>
F/21-38/Domain: transmembrane #status predicted <TMM>
F/39-193/Domain: extracellular #status predicted <EXT>
F/39-10/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C;Accession: F75267
R;Wilte, O; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dc.
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zale, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-153, 'V',155-193 <GOO>
A; Cross-references: GB:L08096; NID:g307127; PIDN:AAA36175.1; PID:g307128
A; Experimental source: B cells
A; Note: sequence extracted from NCBI backbone (NCBIN:131664, NCBIP:131665)
C; Genetics:
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Mismatches:
Indels:
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Matches:
1212 GTGGTCCGAGCAGCAGCCTC 1189
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                                            101 ValValArgAlaAlaAspSerLeu 108
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Query Match:
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probable C2H2-type zinc finger protein F15E12.19 [imported] - Arabidopsis thaliana
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R; Tague, B.W.; Goodman, H.M.
Plant Mol. Biol. 28, 267-279, 1995
Plant Mol. Biol. 28, 267-279, 1995
A; Title: Characterization of a family of Arabidopsis zinc finger protein cDNAs. A; Reference number: S55881; MUID:95322589; PMID:7599312
A; Recession: S55884
                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:AL023496; NID:e1292348; PID:e1292362; PIDN:CAA18912.1.
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C.bate: 02-Mar-2001 #sequence_revision 02-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Comprises: Arabidopsis thaliana (mouse-ear cress)
(.Species: Arabidopsis thaliana (mouse-ear cress)
(.Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jul-2000
                                                                                                                                                          A; Molecule type: mRNA
A;Residues: 1-259 <TAG>
A;Cross-references: GB:L39647; NID:g790678; PIDN:AAA87300.1; PID:g790679
C;Genetics:
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Matches:
Conservative:
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Conservative:
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Gaps:
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JS-09-824-647-16 (1-2095) x H82525 (1-256)
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A;Map position: 1
C;Keywords: DNA binding; zinc finger
C;Keywords: Zinc finger CCHH motif
                                                                  69.9
8.00
100.00%
1.16%
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100.008
1.158
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Best Local Similarity:
Query Match:
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A; Residues: 1-256 <PAR>
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Best Local Similarity:
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Pred. No.:
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uracii-DNA glycosylase XF2692 [imported] - Xylella fastidiosa
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Accession: H82525
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: H82525
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Abauthors: Perreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm Jahuthors: Perreira, V.C.A.; Ferro, J.A.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigrenado, M.A.; Madeira, M.M.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.M.F.; Matchus, E.C.; Miyaki, C.Y.; F.G.; Murtins, E.M.F.; Matchuma, A.Y.; Morck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Murtins, E.M.; M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palnieri, D.P.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A.Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvai, M.F.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GB:AE004075; GB:AE003849; NID:99107929; PIDN:AAF85489.1; GSPDB:GN001
A; Experimental source: strain 9a5c
      , M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Md
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
                                                                                                                                                                                         A;Cross-references: GB:AE001862; GB:AE001825; NID:g6460468; PIDN:AAF12212.1; PID:g64605d
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000
                                                                  A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1. A;Reference number: A75250; MUID:20036896; PMID:10567266 A;Accession: C75611
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                                                                                                                                                                                                                                                                                               A;Map position: 2
C;Superfamily: acetate operon repressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: XF2692
C;Superfamily: uracil-DNA glycosylase
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A; Contents: annotation
C; Genetics:
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Best Local Similarity:
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A; Residues: 1-256 <SIM>
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Best Local Similarity:
                                                                                                                                                      Status: preliminary
                                                                                                                                                                        Molecule type: DNA
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	PIDN:AAL53382.1; PID: M Length:	Score: 8.00		A; Residues: 1-277 < RES> A; Residues: 1-277 < RES> A; Consorreferences: GB:L19182; NID:g307150; PIDN:AAA16187.1; PID:g307151 C; Genetics: A; Gene: MAC25 C; Superfamily: Kazal proteinase inhibitor homology F; 104-156/Domain: Kazal proteinase inhibitor homology < RP18> Alignment Scores: B; 00 Matches: 8 Pred. No.: Csore: 8.00 Matches: 8 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100:00% Mismatches: 0 Ouery Match: 2 DB: Gaps: 0
C;Accession: B96686 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000 R) Huthors: Bunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowakey, D.; Sakano, H. A;Authors: Salaberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Aitle: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Accession: B96686 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-260 csro> A;Cross-references: GB:AE005173; NID:g11038470; PIDN:AAG27749.1; GSPDB:GN00141 C;Genetics: A;Hap position: 1	### Scores: ### 69.8 ###	RESULT 16 TOGGOO	A; Accession: T06600 A; Status: translated from GB/EMBL/DDBJ A; Molecule type: mRNA A; Residues: 1-262 < MIE> A; Remain at language: 1-262 < MIE A; Remain at language: 1-	of biotin mology ase #status prec

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C; Accession: T31146
R; Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, C.W submitted to the EMBL Data Library, July 1998
A; Description: Complete sequence of a 184 kb catabolic plasmid from Sphingomonas aro A; Reference number: 220992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: F83139
R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
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A;Experimental source: strain PAO1
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A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: F83139
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C.Species: Pseudomonas aeruginosa
C.Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: EMBL: AF079317; NID: 93378261; PID: 93378287; PIDN: AAD03870.1
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C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
                                                                                    C.Species: Sphingomonas aromaticivorans
C.Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
                                                  - Sphingomonas aromaticivorans plasmid pNL1
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-293 <ROM>
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A; Residues: 1-295 <STO>
A; Cross-references: GB:
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A; Note: orf181
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A; Accession: A83299
A; Accession: A83299
A; Status: preliminary
A; Aclocule type: DNA
A; Residues: 1-293 <STO>
A; Cross-references: GB:AE004705; GB:AE004091; NID:g9948851; PIDN:AAG06166.1; GSPDB:GN001A; C; Genetics:
A; Genetics:
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Nature 406, 959-964, 2000
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A; Title: Purification and molecular cloning of prostacyclin-stimulating factor from serv A; Reference number: S50031; MUID:95071263; PMID:7980422
A; Accession: S50031
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                                                                                                                                                                                                                                                                                         prostacyclin-stimulating factor - human
C;Species: Homo sapiens (man)
C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 28-May-1999
C;Accession: S50031
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A;Residues: 1-282 <YAN>
A;Cross-references: GBS/55725; NID:g861520; PIDN:AAB32370.1; PID:g861521
A;Cross-references: GBS/55725; NID:g861520 to the concludy of the concluding the concluding the conclude to the concluding the conclude to the concluding the
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                                                                                                                                  LysGlyThrCysGluGlnGlyPro 160
               US-09-824-647-16 (1-2095) x I52825 (1-277)
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Best Local Similarity:
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Tue Jul

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C; Accession: $74694
R; Kaneko, T.; Sato, S.; Kotanl, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajlu
R; Kaneko, T.; Sato, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.;
DNA Res. 3, 109-136, 1996
A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synech
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phosphofructokinase (EC 2.7.1.11) pfkA-2 - Synechocystis sp. (strain PCC 6803) Alternate names: protein sll1196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:281595; PIDN:CAB54304.1; GSPDB:GN00019; CESP:T22H2.6a
A;Experimental source: clone T22H2
                                                                                                             A;Cross-references: EMBL:281595; PIDN:CAB54305.1; GSPDB:GN00019; CESP:T22H2.6b
A;Experimental source: clone T22H2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein T22H2.6a - Caenorhabditis elegans
C;Species: Ceenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T25137
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A;Variety: PCC 6803
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
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Mismatches:
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Mismatches:
                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-345 <MIL>
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A;Molecule type: DNA
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submitted to the EMBL Data Library, November 1996
A:Reference number: Z19985
A:Accession: T25137
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A; Introns: 93/3; 232/3; 314/3
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A; Reference number: 219985
A; Accession: T25138
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Best Local Similarity:
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Best Local Similarity:
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                                                           A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A75000; MID:9969613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Accession: E87929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RibelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, J.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Scl. US.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD325; PMID:11756688
                                                                                                                                                                                                                                                 A; Cross-references: GB:chr_I; PIDN: CABO4752.1; PID: 93880056; GSPDB: GN00019; CESP: T22H2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Species: Brucella melitensis
Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
Accession: AH3282
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Cispedies: Caenorhabditis elegans
Cispedies: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
CiAccession: 725138
Silennard, N.
Submitted to the EMBL Data Library, November 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   primosomal protein N' [imported] - Brucella melitensis (strain 16M)
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Indels:
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Matches:
Conservative:
Mismatches:
Indels:
                   anonymous, The C. elegans Sequencing Consortium.
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                                        Science 282, 2012-2018, 1998
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A; Molecule type: DNA
A; Residues: 1-334 <KUR>
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A; Molecule type: DNA
A; Residues: 1-318 <STO>
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Best Local Similarity:
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Gene: BMEI0245
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Nature 408, 816-820, 2000
A, Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kin
C.A.; Lil, J.H.; Lil, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzi
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A, Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tall
A, Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID: 21016719; PMID: 11130712
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Cjaccession: G69230
Cjaccession: G69230
Cjaccession: G69230
Cjaccession: G69230
Cju, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwan ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: A; Reference number: A69000; MUID: 98037514; PMID: 9371463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gross-references: GB:AE000871; GB:AE000666; NID:92622069; PIDN:AAB85473.1; PID:92
A;Experimental source: strain Delta H
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C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Status: preliminary; nucleic acid sequence not shown; translation not shown
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C.5pecies: Streptococcus pneumoniae
C.5pecies: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
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Conservative:
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C;Superfamily: aspartate aminotransferase
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Score: 8.00 000
Percent Similarity: 100.000
Best Local Similarity: 100.000
Query Match: 1.16%
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A; Residues: 1-387 <STO>
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Best Local Similarity:
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A; Status: preliminary
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Pred. No.:
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Pred. No.:
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A; Note: this species has also been called Salmonella typhi
C; Species: Salmonella enterica subsp. enterica servora Typhi
A; Note: this species has also been called Salmonella typhi
C; Date: 00: Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
C; Accession: AC0972
R; Parkhili, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P; Croin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Parrar, S.; Moule, S.; O'Gaora, P.
A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Atitle: Complete genome sequence of a multiple drug resistant Salmonella enterica servo A; Reference number: AB0502; PMID:11677608
A; Accession: AC0972
A; Residues preliminary
A; Molecule type: DNA
A; Residues: 1-374 cPARA
A; Residues: 1-374 cPARA
A; Residues: 1-374 cPARA
A; Residues: 1-374 cPARA
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: H96652
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hulzar, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - Salmonella enterica subsp. ent
                                                                                                                                           A;Cross-references: EMBL:D90901; GB:AB001339; NID:g1651897; PIDN:BAA16845.1; PID:g165191
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: GB:AL513382; PIDN:CAD03271.1; PID:916504892; GSPDB:GN00176 C; Genetics:
                                                                                                                                                                                                                                          C;Superfamily: 6-phosphofructokinase; 6-phosphofructokinase 1 homology C;Reywords: 91ycolysis; phosphotransferase F;7-313/Domain: 6-phosphofructokinase 1 homology <6PF>
          A; Reference number: S74322; MUID:97061201; PMID:8905231
A; Accession: S74694
A; Status: nucleic acid sequence not shown; translation not shown A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-361 < KAN>
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C;Superfamily: probable hexosyltransferase ytxN
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H96652
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variant surface glycoprotein 7 precursor - Trypanosoma brucei rhodesiense (fragmer
N;Alternate names: metacyclic variable antigen; VSG.
C;Species: Trypanosoma brucei rhodesiense
C;Date: 28-Feb-1986 *sequence_revision 28-Feb-1986 *text_change 17-Nov-2000
                                                                     A; Tille: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58 A; Reference number: AB2577; PMID:11743193
A; Accession: AD3042
A; Status: preliminary
A; Molecule: type: DNA
A; Residues: 1-442 < KUR>
A; Residues: GB. AE008689; PIDN:AAL44754.1; PID:g17742390; GSPDB:GN00187
A; Experimental source: strain C58 (Dupont)
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A,Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: A03393
K; Lenardo, M.J.; Rice-Ficht, A.C.; Kelly, G.; Esser, K.M.; Donelson, J.E. Proc. Natl. Acad. Sci. U.S.A. 81, 6642-6646, 1984
A; Title: Characterization of the genes specifying two metacyclic variable antigen A; Reference number: A94011; MUID:85038570; PMID:6593722
A; Accession: A03393
A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          potasslum channel chain n2P18 homolog - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
C;Accession: T43394
R;Kunkel, M.T.; Salkoff, L.
submitted to the EMBL Data Library, August 1998
A;Description: Potasslum channels in C. elegans.
A;Reference number: 222479
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A;Molecule type: mRNA
A;Residues: 1-461 <KUN>
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A;Map position: linear chromosome
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oxidoreductase Atu3952 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C;Accession: AD3042
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
               Ritetelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidon, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E. Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tunn A;Reference number: A97359; PMID:11743194
A;Accession: H98243
                                                                                                                                                                                                                                                                  A;Residues: 1-434 <KUR>
A;Cross-references: GB:AE005672; PIDN:AAK75500.1; PID:g14972890; GSPDB:GN00164; TIGR:SP4
A;Experimental source: strain TIGR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              agaE protein [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
(Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
C;Accession: H98243
R;Goodher, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Ourollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2333-2338, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: GB: AE007870; PIDN: AAK89474.1; PID: 915159342; GSPDB: GN00170
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A;Molecule type: DNA
A;Residues: 1-442 <KUR>
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C; Accession: C95163
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US-09-824-647-16 (1-2095) x VMUT7R (1-467)

Search completed: July 7, 2003, 15:51:20 Job time: 91.5 secs

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SMS_PETMA
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RS27_METKA
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CLP3_DROME
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ES22_MOUSE
A1AD_HUMAN
YS50_MYCTU
ALXS_ENT
T2D5_RAT
ROXN_HUMAN
                                                DGT1_CERAE
UAP1_ARATH
VSA1_TRYBB
VSI6_TRYBB
YCP7_BRAJA
VSI3_TRYBB
AAT4_ARATH
RRA_FUGRU
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DGT1_HUMAN
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            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

    protein search, using frame_plus_n2p model

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                                                                                                                                                                                                                                                                       112892 seqs, 41476328 residues
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Ygapop 60.0 , Ygapext 6
Fgapop 6.0 , Fgapext
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ALIGNMENTS

Post-processing: Listing first 45 summaries

	J H		OC Mammala; Eutherla; Frimates; Catarrini; Hominidae; Homo. OX NCBL_TaxID=9606; RN [1] RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			KL FICC. Natl. Acad. Sci. U.S.A. 89:1/13-1/19(1994). RN [2] RP REVISIONS, SEQUENCE FROM N.A.	-	_	RP SEQUENCE FROM N.A. RC TISSUEARIAINOPY.			<pre>RL J. Biol. Chem. 267:13073-13078(1992). RN [4] RP SEQUENCE FROM N.A. RC TISSUE-Brain;</pre>
TOTAL COLORES TROUBLES TOTAL T	Command line parameters:	Database : SwissProt_40:*	Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES	Result Query No. Score Match Length DB ID	58.5 593 I GRN_HUMAN P2 4.6 588 I GRN_RAT P2 4.6 589 I GRN_MATTSF P2	591 1 GRN_CAVO P28797 46 1 RNA HORSE BR0030	115 1 VSAB_TRYBB P066177 135 1 YE57_METJA Q58852	181 1 CU25_HUMAN	1.2 212 1 KTHY_HUMAN P23919	H. 2 262 I BCCP_SOYBN Q42783 8 1.2 269 I CITZ_MOUSE 035740	15 17 18

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Best Local Similarity:
Query Match:
Alignment Scores:
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                                                                                                                                                                                        TISSUE-Leukocyte;

XX MEDLINE-91097544; PubMed-2268320;

XX Bateman A. Belcourt D.R., Bennett H.P., Lazure C., Solomon S.;

Bateman A. anovel class of peptide from leukocytes.";

B10chem. Blophys. Res. Commun. 173:1161-1168(1990).

B10chem. Blophys. Res. Commun. 173:1161-1168(1990).

1. FUNCTION: GRANULINS HAYE POSSIBLE CYTOKINE-LIKE ACTIVITY. THEY MAX. PLAX A ROLE IN INTLAMMATION, WOUND REPAIR, AND TISSUE REMODELING.

CELL LINE AA3 IN COUTURE WHILE GRANULIN B ACTS AS AN ANTAGONIST.

TO GRANULIN A, INHIBITING THE GROWTH.

C -1- FUNCTION: GRANULIN A, INHIBITING THE GROWTH.

C -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be produced by alternative splicing.

C -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be produced by alternative splicing.

C -1- TISSUE SPECIFICITY: IN WIELOGENOUS LEUKEMIC CELL LINES OF PROMONOCYTIC, PROWYELOCYTIC, AND PROERTHELIAL CELL LINES. PRESENT CC IN INFLAMMATORY CELLS AND BORE MARROW. HIGHEST LEVELS IN KIDNEY.

C -1- PTM: GRANULINS ARE DISULFIDE BRIDGED.
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ACKGGRANIN
PARAGRANULIN.
GRANULIN 1.
GRANULIN 2.
GRANULIN 3.
GRANULIN 4.
GRANULIN 5.
GRANULIN 7.
N-LINKED (GLCKAC. .) (POTENTIAL).
M-STIKED (GLCKAC. .) (POTENTIAL).
M-SSTIKED (GLCKAC. .) (POTENTIAL).
M-SSTIKED (GLCKAC. .) (POTENTIAL).
M-SSTIKED (GLCKAC. .) (POTENTIAL).
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Cytokine; Repeat; Glycoprotein; Signal; Alternative splicing;
Polymorphism.
        Yu W., Gibbs R.A.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                             Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
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W -> "
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EMBL; AF055008; AAC09359.1; --
EMBL; BC000324; AAH00324.1; --
EMBL; BC010577; AAH10577.1; --
PIR; D36698; D36698.
PIR; JG1284; JG1284.
Genew; HGNC:4601; GRN.
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Pfam; PF00396; granulin; 7.
SMART; SM00277; GRAN; 7.
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                                    Bateman A., Belcourt D.R., Bennett H.P., Lazure C., Solomon S., Granulins, a novel class of peptide from leukocytes. F. Biochem. Biophys. Res. Commun. 173:1161-1168(1990).

-i- FUNCTION: GRANULINS HAYE POSSIBLE CYTORINE-LIKE ACTIVITY. THEY MAY PLAY A ROLE IN INTEMMATION, WOUND REPAIR, AND TISSUE REMODELING.

-I- TISSUE SPECIFICITY: UBIQUITOUS, MOST ABUNDANT IN THE SPLEEN AND SEVERAL TISSUES OF ENDOCRINE SIGNIFICANCE.
                                                                                                                          TGCTGTCCCGCGGGGTTTACGTGTGACACGCAGAAGGGTACCTGTGAACAGGGGCCCCAC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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"The epithelin precursor encodes two proteins with opposing activities on epithelial cell growth.";
J. Biol. Chem. 267:13073-13078(1992).
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01-DEC-1992 (Rel. 24, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Granulins precursor (Acrognain) [Contains: Granulin 1 (Granulin Granulin 2 (Granulin B); Granulin 3 (Granulin B) (Epithelin 2);
Granulin 4 (Granulin A) (Epithelin 1); Granulin 5 (Granulin C);
Granulin 6 (Granulin D); Granulin 7 (Granulin E)].
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"The complementary deoxyribonucleic acid sequence,
distribution, and cellular localization of the rat
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Endocrinology 133:2682-2689(1993).
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MEDLINE-94062640; PubMed-8243292;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 278-328.
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1396 GGGAGCTGGGCCTGCTGCCCCATGCTGTGTGTGCTGCGGAGGATCGCCACCTGC 1455
                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sfb.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     459 GlySerTrpAlaCysCysGlnLeuProHisAlaValCysCysGluAspArgGlnHisCys
                                                                                                                                                                                                                                                                                    ACROGRANIN.
GRANULIN 1.
GRANULIN 2.
GRANULIN 3.
GRANULIN 4.
GRANULIN 6.
GRANULIN 7.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
THEN - SP (IN REF. 2).
TK -> SP (IN REF. 4).
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Sclurognathi; Muridae; Murinae; Mus.
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16-0CT-2001 (Rel. 40, Last annotation update)
Granulins precursor (Acrogranin) [Contains: Granulin 1; Gra
Granulin 3; Granulin 4; Granulin 5; Granulin 6; Granulin 7]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113D434F7E099B31 CRC64;
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Conservative:
Mismatches:
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GRANULINS ARE DISULFIDE BRIDGED.
                                                                                                          or send an email to license@isb-sib.ch)
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MEDLINE-93245991; PubMed-8482392;
                                                                                                                                                                                                                                           PROSITE; PS00799; GRANULINS; 7.
Cytokine; Repeat; Glycoprotein;
                                                                                                                                                                                                      InterPro; IPR000118; Granulin.
Pfam; PF00396; granulin; 7.
SMART; SM00277; GRAN; 7.
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MM.
                                                                                                                                   EMBL; M97750; AAA16903.1; -. EMBL; X62322; CAA44198.1; -.
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PIR; B36199; B36199.
PIR; E36698; E36698.
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Best Local Similarity:
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P28798;
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NCBI_TaxID=10141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    460 GlySerTrpAlaCysCysGlnLeuProHisAlaValCysCysGluAspArgGlnHisCys 479
                                                                TISSUE-Kidney;
MEDLINE-92317004; PubMed-1618805;
Plowman G.D., Green I.M., Neubauer M.G., Buckley S., McDonald V.L.,
Plowman G.D., Green I.M., Neubauer M.G., Buckley S., McDonald V.L.,
Todaro G.I., Shoyab M.;
Todaro G.I., Shoyab M.;
The epithelin precursor encodes two proteins with opposing
activities on epithelial cell growth.";
J. Biol. Chem. 267:13073-13078(1992)
-1- FUNCTION: GRANULINS HAVE POSSIBLE CYTOKINE-LIKE ACTIVITY. THEY MA
PLAY A ROLE IN INRIAMMATION, WONND REPAIR, AND TISSUE REMODELING-
-1- TISSUE SPECIFICITY: UBIQUITOUS.
-1- PTM: GRANULINS ARE DISULFIDE BRIDGED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL). (POTENTIAL). (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
 Baba T., Nemoto H., Watanabe K., Arai Y., Gerton G.L.; "Exon'intron organization of the gene encoding the mouse epithelio/granulin precursor (acrogranin)."; FEBS Lett. 322:89-94(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -> R (IN REF. 2).
1DE8229C413CB787 CRC64;
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GRANULIN 1.
GRANULIN 2.
GRANULIN 3.
GRANULIN 4.
GRANULIN 5.
GRANULIN 6.
GRANULIN 7.
N-LINKED (GLCNAC. ...) (F
N-LINKED (GLCNAC. ...) (F
N-LINKED (GLCNAC. ...) (F
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                           pfam; pr00396; granulin; 7.
SMARF; SM0277; GRAN; 7.
SROSTIE; PS00799; GRANULINS; 7.
Cytokine; Repeat; Glycoprotein; Signal
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P28797;
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DB:
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GRN_CAVPO
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01-DEC-1992 (Rel. 24, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Granulins precursor (Standard Contains: Granulin 1; Granulin 2; Granulin 3; Granulin 4; Granulin 5; Granulin 6; Granulin 7]
                                                                                                                                      Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
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Baba T., Hoff H.B. III, Nemoto H., Lee H., Orth J., Arai Y.,
Gerton G.L.;
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EE7C9FC8F21CB8A1 CRC64;
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GRANULIN 2.
GRANULIN 3.
GRANULIN 4.
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                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND SEQUENCE OF 4-21
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GRANULIN 6.
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InterPro; IPR000118; Granulin.
Pfam; PF00396; granulin; 7.
SMART; SM00277; GRAN; 6.
PROSITE; PS00799; GRANULINS; 6.
CYTOKine; Repeat; Signal; Glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Variant surface glycoprotein ANTAT 1.8 (VSG) (Fragment).
Trypanosoma brucei.
Eukaryota: Euglenozoa: Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_PaxID=5702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         conserved C-terminus.;
Nature 293:230-233(1981).
-I-FUNCTION: THE PARASITE. THE TYPANOSOME EVADES THE IMMONE RESPONSE OF THE HOST BY EXPRESSING
                                                                                                                                                                                                                                                              Infect. Immun. 60:3065-3071(1992).
-1- FUNCTION: HAS ANTIMICROBIAL ACTIVITY AGAINST GRAM-NEGATIVE AND GRAM-POSITIVE BACTERIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SERIES OF ANTIGENICALLY DISTINCT VSGS FROM AN ESTIMATED 1000
                                                                                                                                                                                  TISSUE-Neutrophils;
MEDLINE-92347972; PubMed-1639474;
Couto A.M., Harwig S.S.L., Cullor J.S., Hughes J.P., Lehrer R.I.;
"Identification of eNAP-1, an antimicrobial peptide from equine
                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-82013622; PubMed-7278981;
Matthyssens G., Michiels F., Hamers R., Pays E., Steinert M.;
"Two variant surface glycoproteins of Trypanosoma brucel have a
                                                                                                                                                                                                                                                                                                                                                                                                                           2171934C15265862 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40000
                                                                                                                                                                                                                                                                                                          -1- SIMILARITY: SEEMS TO CORRESPONDS TO GRANULIN 7. Interpro; IPR000118; Granulin. Pfam; PF00396; granulin; 1. SMART; SM00277; GRAN; 1.
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Mismatches:
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13-AUG-1987 (Rel. 05, Last sequence update)
01-MAY-1992 (Rel. 22, Last annotation update)
                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Antimicrobial peptide eNAP-1 (Fragment).
    46 AA.
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 PRT;
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   STANDARD;
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                                                                                           Equus caballus (Horse).
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                                                                                                                                                                                                                                                                                                                                                                                                                         46 AA;
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                                                                                                                                          NCBI_TaxID-9796;
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ENA1_HORSE
P80930;
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P06017;
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noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE-9637999; PubMed-86808087;

MEDLINE-9637999; PubMed-86808087;

MEDLINE-9637999; PubMed-86808087;

MEDLINE-9637999; PubMed-86808087;

MEDLINE-9637999; PubMed-868087;

MILLO G.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinfarotk K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen M.S.M., Weidman J.E., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                              VARIANT SURFACE GLYCOPROTEIN ANTAT 1.8. HYDROPHOBIC, REMOVED DURING MATURATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             snce 273:1058-1073(1996).
SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                      InterPro; IPR001812; Trypan_glycop.
Pfam; PF00913; Trypan_glycop; 1.
Glycoprotein; Antigen; Trypanosomiasis; GPI-anchor; Membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archaea; Euryarchaeota; Methanococci; Methanococcales;
Methanocaldococcaceae; Methanocaldococcus.
NCBL_TaxID-2190;
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                                                                                                                                                                                                                  GPI-ANCHOR.
12761F33D1305C7E CRC64;
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E69A4F18B630A92D CRC64;
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Conservative:
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16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical protein MJ457.
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1s not removed.
agreement (See
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modified and this statement is not remove
entities requires a license agreement (Se
or send an email to license@isb-sib.ch),
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93 115 HY
6 92 92 GP
115 AA; 12530 MW;
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135 AA; 14508 MW;
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                                                                    EMBL; J01227; AAA30292.1;
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                                                                                         PIR; S07326; S07326.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TNE7_HUMAN STANDARD, PRT; 193 AA.
P32970; Q96J57;
Cl-CCT-1993 (Rel. 27, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotati
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                                                                                                             Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R., Horsnell T., Hutchison C.A. III, Kousarides T., Martignetti J.A., Preddie B., Satchwell S.C., Tomlinson P., Weston K.M., Barréal B.G.; Analysis of the protein-coding content of the sequence of human cytomegalovirus strain AD169."; Curr. Top. Microbiol. Immunol. 154:125-169(1990).
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With the control of 
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Bowman M.R., Crimmins M.A., Yetz-Aldape J., Kriz R., Kelleher K.,
Herrmann S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. ..) (POTENTIAL).
57EA40349212FEB8 CRC64;
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Matches:
Conservative:
Mismatches:
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NCBI_TaxID=10360;
                                                                                             SEQUENCE FROM N.A.
MEDLINE-90269039; PubMed-2161319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X17403; CAA35425.1; -.
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Hypothetical protein
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Query Match:
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         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseélsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kochrer K., Beyer A., Mewes H.-W., Gassenhuber J., Wiemann S.;
Submitted (MAX-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9F4831DCEB7DFF2A CRC64;
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Viruses; dSDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181
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Matches:
Conservative:
Mismatches:
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Mismatches:
Indels:
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01-AUG-1990 (Rel. 15, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
Hypothetical protein UL26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein C2lorf25 (Fragment).
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                                                                                                                                                                                                                                                                                                  US-09-824-647-16 (1-2095) x YE57_METJA (1-135)
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                                                                                                                                                                                                                                                                                                                                                                144 GGGACGCCAGCTGTAGCTGC 121
                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AL050173; CAB43307.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 181 AA; 19799 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.2
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Hypothetical protein.
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8.00
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECUENCE FROM N.A.
                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Uterus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UL26_HCMVA
                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CU25_HUMAN
ID CU25_HUMAN
AC Q9Y426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
                                                                                                                                                                                                                                                                                                                                                                                                                                 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P16762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
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UL26_HCMVA
                                                                                                                                                                                                              Query Match:
                                                                                             Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score:
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                                                                                                                                                                          "Molecular cloning and expression of the human deoxythymidylate kinase gene in yeast.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Retrovirus-related Pol. polyprotein from type I retrotransposable element R1 [Contains: Reverse transcriptase (EC 2.7.7.49);
Endonuclease] (Fragment).
Popillia japonica (Japanese beetle).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
                                                                                                                                                        Huang S.H., Tang A., Drisco B., Zhang S.Q., Seeger R., Li C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfan: PF0223; Thymidylate_kin.
Pfan: PF0223; Thymidylate_kin: 1.
TIGRFAMS; TIGR00041; DTMP_kinase; 1.
PROSITE; PS01331; THYMIDYLATE_KINASE; 1.
Transferase; Kinase; Nucleotide biosynthesis; ATP-binding.
NP_BIND 13 20 ATP (PR0BABLE).
CONFLICT 31 CAAGHRA -> SRGPPP (IN REF. 1).
CONFLICT 58 58 Q -> K (IN REF. 2).
                                                                                                                                                                                                                                                                              -i- pathway: Synthesis of dttp from dywp.
-i- Similarity: belongs to the thymidylate kinase Family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-824-647-16 (1-2095) x KTHY_HUMAN (1-212)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic Acids Res. 19:823-827(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105 GCAGCAGGCCACAGGGCAGAACTG
                                         MEDLINE-91204436; PubMed-2017365;
Su J.Y., Sclafani R.A.;
                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-94296549; PubMed-8024690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 i
23902 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X54729; CAA38528.1; -- EMBL; L16991; AAA21719.1; -- PIR; X26845. S26845. HSSP; POG772; 1TWK. Genew; HGNC:3061; DTYKK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.00%
100.00%
1.16%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183
212 AA;
                                                                                                                                                                                                                                                                     5'-diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                             SEQUENCE FROM N.A.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIM; 188345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PO11_POPJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
OB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DAR WEET THE SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CSEEDATAG
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                                                       CTTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
A -> V (IN REF. 1).
9265856833884050 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sytokine; Transmembrane; Glycoprotein; Signal-anchor; Antigen.
                                                                                                                               SUBGNIT: Homotrimer (Probable).
SUBCELLULAR LOCATION: Type II membrane protein.
SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                               -i- SUBGRILGUAR LOCATION: Type - SUBCELLGUAR LOCATION: Type - I- SIBACRIATIY: BELONGS TO THE TUMOR NECKUDING - I- DATABASE: NAME-PROW; NOTE-CD guide CD70 entry; HWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd70.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR.1992 (Rel. 21, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Thymidylate kinase (EC 2.7.4.9) (dTMP kinase)
HOMO sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       212 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-824-647-16 (1-2095) x TNF7_HUMAN (1-193)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1734 CAGGGAGGCCCCGCGCTGGGACGC 1757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlnGlyGlyProAlaLeuGlyArg
                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003637; TNE_7.
InterPro; IPR000478; TNE_family.
Pfam; PP00229; TNE_1.
ProDom; PD036400; TNE_7; 1.
 Immunol. 152:1756-1761(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                154 A
21118 MW;
                                                                                                                                                                                                                                                                                                                                               EMBL; L08096; AAA36175.1; -. EMBL; S69339; AAB30121.1; -.
                                                                                                                                                                                                                                                                                                                                                                        EMBL; BC000725; AAH00725'1;
PIR; A40738; A40738.
Genew; HGNC:11937; TNFSF7.
MIM; 602840; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50049; TNF_1; 1. PROSITE; PS50049; TNF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00207; TNF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity:
                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KTHY_HUMAN
P23919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.:
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 셤
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. -> SI (IN REF. 2). E42876625E61D3CB CRC64;

Conservative: Mismatches: Indels:

Gaps:

82

Length: Matches:

245 AA.

PRT;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-93196484; PubMed-8383793;
MEDLINE-93196484; PubMed-8383793;
Burke W.D., Elckbush D.G., Xiong Y., Jakubczak J.L., Elckbush T.H.;
"Sequence relationship of retrotransposable elements R1 and R2 within and between divergent insect species.";
Mol. Biol. Evol. 10:163-185(1993).
-!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Biotin carboxyl carrier protein of acetyl-CoA carboxylase, chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycine max (Soybean).
Bukaryota, Vildiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermarophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
Scarabaeiformia; Scarabaeidae; Rutelinae; Popillia.
NCBI_TaxID=7064;
                                                                                                                                                                                                                                                                                 PIR; F44490; F44490.
Transferase; RNA-directed DNA polymerase; Transposable element;
                                                                                                                                                                                                                                                                                                                                 REVERSE TRANSCRIPTASE.
NUCLEIC ACID-BINDING ENDONUCLEASE.
44D5C5C55E0D6166 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             245
0
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Matches:
Conservative:
Mismatches:
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Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1494 CTGCGAGAAGGAAGTGGTCTCTGC 1517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168 LeuArgGluGlySerGlyLeuCys 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                        Hydrolase; Nuclease; Endonuclease.
                                                                                                                                                                                                                                                                                                                                 105 RE
245 NU
28406 MW;
                                                                                                                                                                                                                                                                     EMBL; L00944; AAA29783.1; -.
                                                                                                                                                                                                                                                                                                                                                                                              43.1
8.00
100.00%
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                                                                                                                                                                                                                                                                                                                                                         245 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   precursor (BCCP).
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                                                                                                                                                  (DNA)(N)
                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BCCP_SOYBN
Q42783;
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                    DOMAIN
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Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- FUNCTION: Interferes with the binding of transcription factors
-!- FUNCTION: Interferes with the binding of transcription factors
-!- SUBGRILLIA LOCATION: Nuclear.
-!- SUBCELLUIA LOCATION: Nuclear.
-!- ALTERNATIVE PRODUCTS: 4 isoforms; 1 (shown here), 2, 3 and 4; are
produced by alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 3).
MEDILTE-9804278; PubMed-943189;
SALOda T., Fenner M.H., Isselbacher K.J.;
"MSGI and its related protein MRGI share a transcription activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             035740; 035741; 035742; 035743; 055198; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 15-DNN-2002 (Rel. 41, Last annotation update) Cbp/p300-interacting transactivator 2 (MSG-related protein 1) (MRG1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Watsiyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98202510; PubMed-9533950; Dubowoodle S.L.; Rodriguez T.R.; Beddington R.S.P.; Madriguez T.B.; Beddington R.S.P.; Busgl and Mrgl, founding members of a gene family, show distinct patterns of gene expression during mouse embryogenesis.";
                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                       Fatty acid biosynthesis; Biotin; Chloroplast; Transit peptide.
                                                                                                                                                                                                                                                                                                                                                                            BIOTIN CARBOXIL CARRIER PROTEIN
ACETYL-COA CARBOXILASE.
BIOTIN (BY SIMILARITY).
79E273BDBB670F48 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              262
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (1-262)
                                                                                                                                                                                                                                                                                                                                                           CHLOROPLAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1404 CCAGCTCCCACCTGGCTCGGGCA 1381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR001249; Accoa_biotincc.
Interpro; IPR001882; Biotin_attach.
Interpro; IPR000899; Biotin_lipoyl.
Pfam; PF00364; biotin_lipoyl.
PRINTS; PR01071; ACOABIOTINCC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-824-647-16 (1-2095) x BCCP_SOYBN
                                                                                                                                                                EMBL; U40666; AAB67836.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                    227 B
                                                                                                                                                                                                                                                                                                  TIGRFAMS; TIGR00531; BCCP; 1. PROSITE; PS00188; BIOTIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42.6
8.00
100.00%
100.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene 204:235-241(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITED OR MRG1 OR MSG2.
                                                                                                                                                                                                                                                                                                                                                                              262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-C57BL/6 X DBA;
                                                                                                                                                                                                                                                                                                                                                                                                                                       262 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                    227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                     P02905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CIT2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein)
                                                                                                                                                                                                                                                                                                                                                           RANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                      BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
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Ю
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CIT2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
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InterPro; IPR000980;
                                                                                                                                                                        DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                   Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                       073612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus
                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                   EFB1_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EFNB1
                                                                                                                                                                                                                                                                                                                                                                       RESULT 16
                                                                                                                                                                                                                                  Score:
                                                                                                                                                                                                                      Pred.
                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoldea; Pipidae;
                                                                                                                                                                                   Nuclear protein; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASP/GLG-RICH (ACIDIC).
MISSING (IN ISOFORM 2).
MISSING (IN ISOFORM 3).
MISSING (IN ISOFORM 4).
7: AFACDDD5D7902A48 CRC64;
                                                                                                                                                                                                                                                                                                  7
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
SH2/SH3 adaptor crk (Adapter molecule crk) (CRK2).
                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         296 A.A.
-!- SIMILARITY: BELONGS TO THE CITED FAMILY
                                                                                                                                                                                                                                                                                                                                               Indels:
                                                                                                                                                                                                                                                                                                                                                                               US-09-824-647-16 (1-2095) x CIT2_MOUSE (1-269)
                                                                                                                                                                                                                                                                                                                                                                                                       1231 GCTGGGGGCAGCAGTGCTGGTGGT 1208
                                                                                                                                                                                             HIS-RICH.
GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                  186 AlaGlyGlySerSerAlaGlyGly 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                 28382 MW;
                                                                                                               EMBL; Y15163; CAA75432.1; -.
                                                                                                                                                             AAC39945.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U89774; AAB49698.1; -.
HSSP; Q64010; 1CKA.
                                                                                                                                                EMBL; Y15163; CAA75435.1; -.
                                                                                                                                                                                                                                                                                                                      100.008
100.008
1.168
                                                                                                                          EMBL; Y15163; CAA75433.1
EMBL; Y15163; CAA75434.1
                                                                                                                                                                                                                                                                                                  42.5
                                                                                                                                                                      MGD; MGI:1306784; Cited2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                        159 2
203 2
269 AA;
                                                                                                                                                                                                                                                                                                                                    Best Local Similarity:
                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                  Transcription
                                                                                                                                                                                                                                                                                      Alignment Scores:
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P87378;
                                                                                                                                                                                                                                                     VARSPLIC
SEQUENCE
                                                                                                                                                                                                                             VARSPLIC
                                                                                                                                                                                                                                          VARSPLIC
                                                                                                                                                                                                                                                                                                                                             Query Match:
DB:
                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                          DOMAIN
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                                                                                                                                                                                                                                                                                                  Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRK_XENLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phaslanidae; Phaslaninae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Reciprocal expression of the Eph receptor Cek5 and its ligand(s) in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dev. Biol. 182:256-269(1997).

-1- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASE EPHB2.

-1- SUBCELLULAR LOCATION: Type I membrane protein.

-1- TYROPIASMIC PHOSPHORYLATION TYPE I THE
CYTOPIASMIC DOWAIN (BY SIMILARITY).
                                                                                                                                                a His
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-97223524; PubMed-9070326;
Hellash J.A., Soans C., Chong L.D., Shao H., Dixit V.M.,
Pasquale E.B.
                                                                                                                                                                                                                                                                                                                                                                                                544F11F4A1F75A66 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-CCT-2010 (Rel. 40, Last annotation update)
Ephrin-B1 precursor (CEK5 ligand) (CEL5-L).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       334 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-824-647-16 (1-2095) x CRK_XENLA (1-296)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 ArgProProSerSerProGlySer 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40 AGGCCACCCAGCTCACCAGGGTCC 17
                                                                                                                                                                                                                                                                                                                                                 SH3 1.
SH3 2.
                                                                                                                                                                                                                                     PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 1.
SH2 domain; Repeat.
DOMAIN 13 112 SH
                                                                                                                                                                                                                                                                                                                                               125 185 S
249 289 S
296 AA; 33409 MW;
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Pfam; PF00812; Ephrin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin; 1.
                                                                     PRINTS; PRO0401; SH2DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
ProDom; PD000066; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.00%
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                                                                                                                         Prodom; PD000066; SH3; 1.
Prodom; PD000093; SH2; 1.
SMART; SM00252; SH2; 1.
SMART; SM00326; SH3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.8
                   Pfam; PF00017; SH2; 1.
Pfam; PF00018; SH3; 1.
InterPro; IPR001452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aliqnment Scores:
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96A83E05F318552C CRC64;

38588 MW;

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361 AA;
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     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 18
NPT4_HUMAN
                                                                                                                Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THE HEAVE BEEN SOCOCOCCE SERVER SERVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
PROSITE; PS01299; EPHRIN; 1.
Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;
Signal; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
PLINKED (GICNAC.).
N-LINKED (GICNAC.).
N-RESSEESEDSCOPS CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
6-phosphofructokinase (EC 2.7.1.11) (Phosphofructokinase)
                                                                                                                                         EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chrococcales; Synechocystis.
                                                                                                                                                                                                                                                                                                                                                            334
0
0
0
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PRINTS; PR00476; PHFRCTKINASE.
PRODM; PD000707; Ppfruckinase; 1.
PROSITE: PS00433; PROSPHORRUCTOKINASE; 1.
Kinase; Transferase; Glycolysis; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-824-647-16 (1-2095) x EFB1_CHICK (1-334)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                        POTENTIAL.
                                                                                                                      EPHRIN-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTCGATGGCTCCTGGGGGTGCTG 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 GlyArgTrpLeuLeuGlyValLeu 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                               334 CX
334 PL
135 N-
36858 MW;
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                                                                                                                                                                                                                                                                                                                                                            41.1
8.00
100.00%
100.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Phosphohexokinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                              334 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFKA OR SLL1196
                                                                                                                   26
23
232
253
332
135
                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            K6PF_SYNY3
P72830;
                                                                                                                CHAIN
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
                                                                                                                                                                                                  DOMAIN
                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transport; Symport; Sodium transport; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                        Bikaryota; Metazoa; Chordata; Cranlata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                               15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
50dlum-dependent phosphate transport protein 4 (Sodlum/phosphate cotransporter 4) (Na(+)/PI cotransporter 4).
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                                                                           54.5
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52359B2091948285 CRC64;
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Matches:
Conservative:
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N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
                                             Conservative:
Mismatches:
                                                                                                                                                                                                                                                                      401 AA.
               Length:
Matches:
                                                                                  Indels:
                                                                                                                                  US-09-824-647-16 (1-2095) x K6PF_SYNY3 (1-361)
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POTENTIAL.
POTENTIAL.
                                                                                                    Gaps:
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                                                                                                                                                                1152 TTGGCAGCAGGTATCGGAGGAGGG 1129
                                                                                                                                                                                   193 LeuAlaAlaGlyIleGlyGlyGly 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39.9
8.00
100.00%
               40.6
8.00
100.00%
100.00%
1.16%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U90545; AAB53423.1; -
Genew; HGNC:10931; SLC17A3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44051
                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                        Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIM: 604216;
Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores
                                                                                                                                                                                                                                                                        NPT4_HUMAN
000476;
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RECEIVED TO COLUMBIA;

REDINE-21016719; PubMed-11130712;

RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

RA Theologis A., Cana A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA White O., Alonso J., Chonway A.B., Conway A.R., Creasy T.H., Dewar K.,

Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

RA Lin J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

RA Langin-Hooper S., Lee A., Lee J.W., Lenz C.A., Li J.H., Li Y.-P.,

RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

RA Bai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,

Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

RA Wu D., Yu G., Fraser C.M., Venber J.C., Davis R.W.;

Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               I- FUNCTION: IMPORTANT FOR THE METABOLISM OF AMINO ACIDS AND KREBS-CYCLE RELATED ORGANIC ACIDS. IN PLANTS, IT IS INVOLVED IN NITROGEN METABOLISM AND IN ASPECTS OF CARBON AND ENERGY METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: L-aspartate + 2-oxoglutarate = oxaloacetate +
                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thallana (Mouse-ear cress).

Eukaryota, Viridiphantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAUTION: Ref.2 sequence differs from that shown due to erroneous gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: HOMODIMER (BY SIMILARITY).
SUBCELLULAR LOCATION: Cytoplasmic (Potential).
SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schultz C.J., Coruzzi G.M.; "The aspartate aminotransferase gene family of Arabidopsis encodes isoenzymes localized to three distinct subcellular compartments.";
                                                                                                                                                                                                                                                                                                                     15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Aspartate aminotransferase, cytoplasmic isozyme 2 (EC 2.6.1.1)
    000
  Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                   (Transaminase A).
ASP4 OR AT1G62800 OR F23N19.17 OR F23N19_26.
                                                                                                                                                                                                                                                           403 AA.
                          Indels:
                                                                                      US-09-824-647-16 (1-2095) x NPT4_HUMAN (1-401)
                                              Gaps:
                                                                                                                                                      281 ProSerSerAlaLeulleValSer 288
                                                                                                                                CCATCCAGTGCCCTGATAGTCAGT 403
                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-cv. Columbia; TISSUE-Leaf;
MEDLINE-97201829; PubMed-7894512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COFACTOR: PYRIDOXAL PHOSPHATE
                                                                                                                                                                                                                                                                             P46646; 098169;
01-NOY-1995 (Rel. 32, Created)
15-UNN-2002 (Rel. 41, Last and
15-JUN-2002 (Rel. 41, Last and
    100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 408:816-820(2000).
                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant J. 7:61-75(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMINOTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBL_TaxID=3702;
                                                                                                                                                                                                                                                   AAT4_ARATH
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                        Query Match:
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and for commercial
              entities requires a license agreement (See http://www.lsb-slb.ch/announce/or send an email to license@lsb-slb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
-1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
NR1 SUBFAMILY.
                                                                                                                                                              Interpro;
Interpro;
Pfam; PF00155; aminotran_1_2; 1.
PRINE; PRO0155; aminotran_1_2; 1.
PRINE; PS00105; AA_TRANSER_CLASS_1; 1.
PROSITE; PS00105; AA_TRANSFRER_CLASS_1; 1.

"""" FPCSTE; PS00105; AA_TRANSFRER_CLASS_1; 1.

"""" PROSITE; PS00105; AA_TRANSFRER_CLASS_1; 1.

""" FPCSTER_CLASS_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- SUBCELLULAR LOCATION: Nuclear.
-i- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA-1 (SHOWN HERE) AND ALPHA-2; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- FUNCTION: THIS IS A RECEPTOR FOR RETINOIC ACID. THIS METABOLITE HAS PROFOCUND EFFECTS ON VERTEBRATE DEVELOPHENT. RETINOIC ACID IS A MORPHOGEN AND IS A POWERFUL TERATOGEN. THIS RECEPTOR CONTROLS CELLS FUNCTIONS BY DIRECTLY REGULATING GENE EXPRESSION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chatterjee K.K.; raid of the retinoic acid receptor-alpha "Isolation and characterization of the retinoic acid receptor-alpha gene in the Japanese pufferfish, F. rubripes."; Gene 236:315-323(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wentworth J.M., Schoenfeld V., Meek S., Elgar G., Brenner S.,
                                                                                                                          :ME
þ
                                                                                                                                                                                                                                                                                                                                                                                       80000
                                                                                                                                                                                                                                                                                                                                                                                                         Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Retinoic acid receptor alpha (RAR-alpha).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            447 AA.
  modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                       Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels:
                                                                                                                                                                                                                                                                                                                                                                   Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-824-647-16 (1-2095) x AAT4_ARATH (1-403)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               465 GGGCCACCCCCAGGAGCCATC 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR004839; Aminotransf1/2.
                                                                                              AC007190; AAF19543.1; ALT_SEQ P00508; 7AAT.
                                                                                                                                                    IPR000796; Asptransf_sub.
IPR004838; NHtransf_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-99384012; PubMed-10452951;
                                                                                                                                                                                                                                                                                                                                                                                                     rercent Similarity: 100.008
Best Local Similarity: 100.008
Query Match: 1.168
                                                                            EMBL; U15035; AAA79372.1
                                                                                                                                                                                                                                                                                                                                                                   6.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=31033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RRA_FUGRU
Q9W5Z3; Q9W5Z4;
                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                        InterPro;
                                                                                                                  HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 20
a
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Trypanosomiasis; GPI-anchor; Membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE-98434592; PubMed-9756920;
                                                                                                                       49963 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF059202; AAC63997.1;
                                                                                                                                                                         8.00
100.00%
100.00%
1.16%
                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HGNC:2843; DGAT1
                           88
444
467
1108
252
416
444
  Antigen;
                                                                                                                      467 AA;
                                                                                                                                                                                                    Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-9606;
  Glycoprotein;
NON_TER
NON_CONS 8
                                                                                                                                                                                          Percent Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM; 604900;
                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                    DGT1_HUMAN
075907;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                    CARBOHYD
CARBOHYD
                                                                                                                      SEQUENCE
                                                                                                CARBOHYD
                                           CHAIN
                                                                                                                                                                 Pred. No.:
                                                                                                                                                                                                                                                                                                                                                         GT1_HUMAN
                                                                                                            LIPID
                                                                                                                                                                                                                                                                                                                                            RESULT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SELLELEES
                                                                                                                                                                                                                                                                                                                                               LIGAND-BINDING.
MAGKGNPVPGPHLNGFPVPTYSYFFPHMLGSLSPPALPGLP
                                                                                                                                                                                                                                                                                                                                                                       ISGYSTPSPAT -> MYESVDVVGLNPSPNPFLMMETYNQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma
NCBI_TaxID=31286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDINE-85038570; PubMed-6593722;
Lenardo M.J., Rice-Ficht A.C., Kelly G., Esser K.M., Donelson J.E.;
Characterization of the genes specifying two metacyclic variable antigen types in Trypanosoma brucei rhodesiense.";
Proc. Natl. Acad. Sci. U.S.A. 81:6642-6646(1984)
-!-FUNCTION: VGG FORMS A CORT ON THE SURFACE OF THE PARASITE. THE TYPANOSOME BYADES THE IMMUNE RESPONSE OF THE HOST BY EXPRESSING A SERIES OF ANTIGENICALLY DISTINCT VSGS FROM AN ESTIMATED 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
11-DEC-1998 (Rel. 37, Last annotation update)
Variant surface glycoprotein 7 (VSG 7) (Metacyclic variable antigen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor. A SOLUBLE FORM IS RELASED FROM RUPTURED CELLS BY THE ACTION OF
                                                                                                                                                                                                                                                                                                                                                                                     RGCLIPEKGLVPGAPHPYSTSIRNOHWNGSNHS (IN
                                                                                                                                                                                                                                   PROSITE; PS00031; NUCLEAR RECEPTOR; 1. Receptor; Transcription regulation; DNA-binding; Nuclear protein; Zinc-finger; Multigene family; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                   [SOFORM ALPHA-2].
E00630F720B1508D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     447
8
0
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0
0
                                                                                                                                                                                                                                                                                         NUCLEAR RECEPTOR-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           467 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (1-447)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MODULATING
         to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                        C4-TYPE.
C4-TYPE.
                                EMBL; AJ012382; CAB96754.1; --
EMBL; AJ012380; CAB96754.1; JOINED.
EMBL; AJ012381; CAB43979.1; --
EMBL; AJ012380; CAB43979.1; JOINED.
EMBL; AJ012378; CAB43870.1; --
EMBL; AJ012379; CAB43871.1; --
HSSP; P10826; 1HRA.
                                                                                                                             InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001628; Znf_C4steroid.
                                                                                                                                                                               PRINTS; PR00047; STROIDFINGER.
ProDom; PD000035; Znf_C4steroid; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD; PRT;
                                                                                                                                                                                                                                                                                                                                   HINGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-824-647-16 (1-2095) x RRA_FUGRU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Fragments).
Trypanosoma brucei rhodesiense.
                                                                                                                                                       Pfam; PF00104; hormone_rec; 2. Pfam; PF00105; zf-C4; 2.
                                                                                                                                                                                                                                                                                                                                                                                                               49532 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        39.3
8.00
100.00%
100.00%
1.16%
                                                                                                                                                                                                                         C4: 1.
                                                                                                                                                                                                              SMART; SM00430; HOLI;
SMART; SM00399; ZnF_C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A03393; VMUT7R.
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Best Local Similarity:
Query Match:
           email
                                                                                                                                                                                                                                                                                                                                                                                                                 447
                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
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ID VSG7_TRYBR
AC P02898;
            an
                                                                                                                                                                                                                                                                                             DNA_BIND
ZN_FING
                                                                                                                                                                                                                                                                                                                                                  DOMAIN
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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DOMAIN
           or send
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             triacylglycerol.
-!- PATHWAY: Central role in the metabolism of cellular diacylglycerol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acyl
InterPro; IPR002688; ACAT.
Pfam; PF01800; ACAT; 1
Pfam; PF01800; ACAT; 1
Pfam; PF01800; ACAT; 1
PF01800; ACYltransferase; Transmembrane; Endoplasmic reticulum.
TRANSMEM 104 124
PRANSMEM 100 150
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sturley S.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 reticulum (By similarity).
SIMILARITY: BELONGS TO THE STEROL O-ACYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-0cr-2001 (Rel. 40, Created)
16-0cr-2001 (Rel. 40, Last sequence update)
16-0cr-2002 (Rel. 40, Last sequence update)
Diacylglycerol 0-acyltransferase 1 (EC 2.3.1.20) (Diglyceride acyltransferase) (ACAT related gene product 1).
DGAIL OR DGAT OR ACRP!
HOMO saplens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - COA +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- CATALYTIC ACTIVITY: Acyl-CoA + 1,2-diacylglycerol
                                                                                                                                                         GPI-ANCHOR.
3A4805AFFBECA686 CRC64;
                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     488 AA
                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-824-647-16 (1+2095) x VSG7_TRYBR (1-467)
                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1632 GCCCTGTCGGTTGTCTCGGCAGCA 1609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                454 AlaLeuServalvalSerAlaAla 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- PATHWAY: Central role in the metabolism of cellular diacylglycerol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Joyce C.W., Davis M.A., Anderson R.A., Rudel L.L.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Catalyzes the terminal and only committed step in
triacylglycerol synthesis by using diacylglycerol and fatty acyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane; Endoplasmic reticulum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cercopithecus aethiops (Green monkey) (Grivet).
Wakaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reticulum (By similarity).
-i- SIMILARITY: BELONGS TO THE STEROL O-ACYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Diacylglycerol O-acyltransferase I (EC 2.3.1.20) (Diglyceride
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: Acyl-CoA + 1,2-diacylglycerol = CoA +
                                                                                                       12E34BA7478ABA1F CRC64;
                                                                                                                                                                   Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                  491 AA.
                                                                                                                                                                                                             Indels:
                                                                                                                                                     Length:
                                                                                                                                                                                                                                                        US-09-824-647-16 (1-2095) x DGT1_HUMAN (1-488)
                                                                                                                                                                                                                                Gaps:
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                                                                                           POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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InterPro; IPR002688; ACAT.
Pfam; PF01800; ACAT; 1.
                                                                                                       55252 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Acyltransferase;
                                                                                                                                                38.7
8.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CoA as substrates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   triacylglycerol.
                                            332
406
428
453
488 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                              Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acyltransferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-9534;
                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DGAT1 OR DGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ransferase;
                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                 DGT1_CERAE
Q9GMF1;
                                                           TRANSMEM
TRANSMEM
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SEQUENCE
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9
                                                                                                                                                                                                                                                                                                                                                                 DGT1_CERAE
                                                                                                                                                                                                                                                                                                                                                   RESULT 23
                                                                                                                                                                   Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 402:761-768(1999).
-I- CATALYTIC ACTIVITY: UTP + N-acetyl-alpha-D-glucosamine 1-phosphate
- dlphosphate + UDP-N-acetyl-D-glucosamine.
-I- PATHWAY: UDP-GlCNAc blosynthesis from Fru-6-P; fourth (last)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-CV. Columbia;
MEDLIKE-20083487; PubMed-10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
Moffat K.S., Cronin L.A., Shen M., Pal G., Van Aken S., Umayam L.,
Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
Goodman H.M., Somerville C.R., Copenhaver G.P., Freuss D.,
Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Probable UDP-N-acetylglucosamine pyrophosphorylase (EC 2:7.7.23).
AT2G35020 OR F1913.25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.",
                                                                                                              250
                  POTENTIAL.
BFD3683453D588DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72C0F2DCF15ACAD7 CRC64;
                                                                                                                           Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                             PRT; 502 AA.
                                                                                          Length:
Matches:
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                                                                                                                                                                               Gaps:
   POTENTIAL
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                                                                                                                                                                                                                                                                  15 ThrGlySerArgProSerSerHis 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleotidyltransferase.
                                                                                                                                                                                                                                                  1417 ACTGGCAGCAGGCCCAGCTCCCAC
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                                      55643 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55759 MW;
                                                                                   38.7
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Pfam; PF01704; UDPGP; 1.
Transferase; Nucleotidyltra
                                                                                                                                                                                                                                                                                                                                     STANDARD;
   451
476
 431 4
456 4
491 AA;
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502 AA;
                                                                                                                         Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137
                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venter J.C.
                                                                                                                                                                                                                                                                                                                                                           UAP1_ARATH
064765;
TRANSMEM
TRANSMEM
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ACT_SITE
SEQUENCE
                                      SEQUENCE
                                                                                                                                                              Query Match:
                                                                                                                                                                                                                                                                                                                                          UAP1_ARATH
                                                                                                                                                                                                                                                                                                                        RESULT 24
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38.5

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITYPANOSOME bruce1: The extent of conversion in antigen genes may I related to the DNA coding specificity.";
Cell 42:821-829(1985).
-- FUNCTION: VGG FORMS A COAT ON THE SURFACE OF THE PARASITE. THE -- FUNCTIONS WADDES THE IMMUNE RESPONSE OF THE HOST BY EXPRESSING A SERIES OF ANTIGENICALLY DISTINCT VSGS FROM AN ESTIMATED 1000
                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 270-344 FROM N.A.
MEDILINE-86028178; PubMed-4053185;
Bays E., Bouard S., Pays A., van Assel S., Dupont F., Aerts D.,
Huet-Duviller G., Gomes V., Richet C., Degand P., van Meirvenne N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor. A SOLUBLE FORM IS RELASED FROM RUPTURED CELLS BY THE ACTION OF
                                                                                                                                                                                                                                                                                     13-AuG-1987 (Rel. 05, Created)
13-AuG-1987 (Rel. 05, Last sequence update)
13-AuG-1987 (Rel. 39, Last annotation update)
30-WAY-2000 (Rel. 39, Last annotation update)
Variant surface glycoprotein AnTaT 1.1 precursor (VSG) (Expression-linked copy) (ELC).
Trypanosoma brucei brucei.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIINE-84028590; PubMed-6313354;
Michiels F., Matthyssens G., Kronenberger P., Pays E., Dero B.,
van Assel S., Darrille M., Cravador A., Steinert M., Hamers R.;
Gene activation and re-expression of a Trypanosoma brucei variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Steinert M., Pays E.;
programming of antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-82013622; PubMed-7278981;
Matthyssens G., Michiels F., Hamers R., Pays E., Steinert M.;
"Two variant surface glycoproteins of Trypanosoma brucei have
80000
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                    503 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            van der Werf A., van Assel S., Aerts D., "Telomere interactions may condition the
                                                     Indels:
                                                                                                       US-09-824-647-16 (1-2095) x UAP1_ARATH (1-502)
                                                                         Gaps:
                                                                                                                                          242 TCTCAGGGACTTCCAGTTGCTGCC 265
                                                                                                                                                          82 SerGinGlyLeuProValalaAla 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expression in Trypanosoma brucei.";
EMBO J. 9:1035-1040(1990).
                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-90214610; PubMed-2323332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-416 FROM N.A.
 8.00
100.00%
100.00%
1.15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          surface glycoprotein.";
EMBO J. 2:1185-1192(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wature 293:230-233(1981).
                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        conserved C-terminus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-EATRO 1125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                      Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=5702;
                                                                                                                                                                                                                                                                         026722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Steinert M.;
                                                                                                                                                                                                                                                        VSA1_TRYBB
P06015; Q26
                                                       Query Match:
                                                                                                                                                                                                                     RESULT 25
VSA1_TRYBB
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EMBL; X01843; CAA25971.1;

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                                                                                      WARIANT SURFACE GLYCOPROTEIN ANTAT 1.1.
HYDROPHOBIC, REMOVED DURING MATURATION.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
GPI-ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; S09640; S09640.
InterPro; IPR001812; Trypan_glycop.
Pfam; PF00913; Trypan_glycop; 1.
Glycoprotein; Antigen; Trypanosomiasis; Signal; GPI-anchor; Membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-Aug-1987 (Rel. 05, Created)
13-Aug-1987 (Rel. 05, Last sequence update)
01-MAY-1992 (Rel. 22, Last annotation update)
Variant surface glycoprotein ILTAT 1.3 precursor (VSG).
Trypanosoma brucei brucei.
Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rice-Picht A.C., Chen K.K., Donelson J.E.;
Sequence homologies near the C-termini of the variable surface glycoproteins of Trypanosoma brucei.";
Nature 294:33-57(1981).
1- FUNCTION: VSG FORMS A COAT ON THE SURFACE OF THE PARASITE. THE TYPANOSOME EVADES THE IMMUNE RESPONSE OF THE HOST BY EXPRESSING A SERIES OF ANTIGENICALLY DISTINCT VSGS FROM AN ESTIMATED 1000
                                                                       Antigen; Trypanosomiasis; GPI-anchor; Membrane; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor. A SOLUBLE FORM IS RELASED FROM RUPTURED CELLS BY THE ACTION OF PI-PLC.
                                                                                                                                                                                                                   -> P (IN REF. 2).
-> V (IN REF. 2).
-> K (IN REF. 3).
38541B93F6DF46C6 CRC64;
                                                                                                                                                                                                                                                                                                        8
0
0
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     503 AA.
                                                                                                                                                                                                                                                                                                                        Matches:
                                                                                                                                                                                                                                                                                                        Length:
                                                                                                                                                                                                                                                                                                                                                                                                       US-09-824-647-16 (1-2095) x VSA1_TRYBB (1-503)
                                                                                                                                                                                                                                                                                                                                                               Indels:
                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; S07174; VMUT1B.
InterPro; IPR001812; Trypan_glycop.
Pfam; PF00913; Trypan_glycop; 1.
                                                                                                                                                                                                                        KKZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; J01221; AAA30288.1; -.
                                                                                                                                                                                                                                                                  Ĕ
                     EMBL; J01213; AAA30280.1; -.
                                                                                                                                                                                                                                                                                                     38.5
8.00
100.00%
100.00%
1.16%
                                                                                                                                                                                                                                                                  52814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                        480
503
172
209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=5702;
                                                                               Glycoprotein;
SIGNAL
                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 26
VSI6_TRYBB
ID VSI6_TRYBB
AC P06014;
                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                        CONFLICT
                                                                                                                                        DISULFID
                                                                                                                                                  DISULFID
                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                         CONFLICT
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Q
                                                                                                             CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tully R.E., van Berkum P., Lovins K.W., Keister D.L.;
"Identification and sequencing of a cytochrome P450 gene cluster from Bradyrhizobium japonicum.";
Blochim. Blophys. Acta 1398-243-255(1998).
-1- SIMILARITY: CONTAINS 2 PFTB REPEATS.
          VARIANT SURFACE GLYCOPROTEIN ILTAT 1.3.
HYDROPHOBIC, REMOVED DURING MATURATION.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Bradyrhizobium group; Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-USDA 110;

Tully R.E., Keister D.L.;

"Cloning and mutagenesis of a cytochrome P-450 locus from

Bradyrhizoblum japonicum that is expressed anaerobically and

symbiotically.";
                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 55.4 kDa protein in CYP117 3'region (ORF7).
                                                                                                                  70144D8B0408AA9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8C0660A0C7AFBCE5 CRC64;
                                                                                                                                                                                           Conservative:
Mismatches:
Indels:
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Appl. Environ. Microbiol. 59:4136-4142(1993).
                                                                                                                                                                                                                                                                                                                                                                                       516 AA.
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Matches:
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Matches:
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                                                                                                    GPI-ANCHOR
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PFTB 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 35, Created)
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REPEAT 45 86
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                                                                                                                                                             38.5
8.00
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                                                                                                                  503 AA;
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                                                                                                                                                                                                         Best Local Similarity:
Query Match:
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Best Local Similarity:
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                                                                                                                                                                                           Percent Similarity:
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01-NOV-1997
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                                         DISULFID
                                                                       CARBOHYD
CARBOHYD
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                                                                                                                                                                                                            01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Variant surface glycoprotein ILTAT 1.23 precursor (VSG).
Trypanosoma brucei brucei.
Bukaryota: Buglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TAXID-5702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSG GENES.
-1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
A SOLUBLE FORM IS RELASED FROM RUPTURED CELLS BY THE ACTION OF A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein; Antigen; Trypanosomiasis; GPI-anchor; Membrane; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT SURFACE GLYCOPROTEIN ILTAT 1.23
                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Variant specific glycoprotein of Trypanosoma brucel consists of two domains each having an independently conserved pattern of cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYDROPHOBIC, REMOVED DURING MATURATION.
N-LINKED (GLCNAC. . . ) (POTENTIÁL).
N-LINKED (GLCNAC. . . ) (POTENTIÁL).
N-LINKED (GLCNAC. . . ) (POTENTIÁL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. MOL. Biol. 221:823-835(1991).
-!- FUNCTION: YGG FORMS A COAT ON THE SURFACE OF THE PARASITE. THE
- TYPANOSOME EVADES THE IMMURE RESPONSE OF THE HOST BY EXPRESSING
A SERIES OF ANTIGENICALLY DISTINCT VSGS FROM AN ESTIMATED 1000.
                                                                                                            St.
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-ISOJAte MIAZ 206;
MEDLINE-92046637; Pubmed-1942032;
Carrington M., Miller N., Blum M.L., Roditi I., Wiley D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPI-ANCHOR (BY SIMILARITY).
EEDOD72C919396E6 CRC64;
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                                                    US-09-824-647-16 (1-2095) x YCP7_BRAJA (1-516)
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                                                                                                       US-09-824-647-16 (1-2095) x VSI3_TRYBB
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532 AA;
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Best Local Similarity:
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P26328;
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RESULT 29

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064176
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                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                    BY SIMILARITY.

LIVER CARBOXYLESTERASE 3.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . . ) (POTENTIAL).
                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Liver carboxylesterase 3 precursor (EC 3.1.1.1) (Carboxyesterase ES-3)
(PI 5.5 esterase) (ES-HTEL).
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                            -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                     -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)0 - an alcohol + a
                                                                                                                                                                                                                        -1 - SUBCELLULAR LOCATION: Microsomal membrane, lumen of endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00135; COesterase; 1.
PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
PROSITE; PS00441; CARBOXYLESTERASE_B_2; 1.
Glycoproteal; Hydrolase; Serine esterase; Endoplasmic reticulum; signal; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LINKED (GLCNAC. . .) (P
1E14D66DF089B86F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        561
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Conservative:
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            561 AA.
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InterPro; IPR000379; Ser_estrs_site.
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            PRT;
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8.00
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            STANDARD;
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221
466
116
284
561
                                                                                                                                                                                                                   carboxylic anion
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                                                                                                                             SEQUENCE FROM N.A.
                                                                                                         NCBI_TaxID=10116;
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Best Local Similari
                                                                                                                                                                                                                                       reticulum
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ACT_SITE
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                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-92147141; PubMed-1783403;
Ovnic. M., Swaink R.T., Fletcher C., Zhen L., Novak E.K., Baumann H.,
Heintz N., Ganschow R.E.,
"Characterization and functional expression of a cDNA encoding egasyn
(esterase-22); the endoplasmic reticulum-targeting protein of beta-
qlucuronidase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                   glucuronidase..;
Genomics 11:956-967(1991).
--- FUNCTION: INVOLVED IN THE DETOXIFICATION OF XENOBIOTICS AND IN
THE ACTIVATION OF ESTER AND AMIDE PRODRUGS.
--- CATALYTIC ACTIVATY: A carboxylic ester + H(2)0 - an alcohol + a
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Liver carboxylesterase 22 precursor (EC 3.1.1.1) (Egasyn) (Esterase-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- SUBCELLULAR LOCATION: Microsomal membrane, lumen of endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PREVENT SECRETION FROM ER (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                 Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PSOU12; CARBOXYLESTERASE B 1; 1.
PROSITE; PSO0941; CARBOXXLESTERASE B 2; 1.
Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIVER CARBOXILESTERASE 22.
BY SIMILARITY.
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PREVENT SECRETION FROM ER (F
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FB1A4367A0CCB2E3 CRC64;
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Matches:
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InterPro; IPR000379; Ser_estrs_site.
Pfam; PF00135; COesterase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 GTGGCCTTAACAGCAGGGCTGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            carboxylic anion;
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562 AA;
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                    NCBI_TaxID-10090;
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Pred. No.:
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AAB60351.1; AAB59487.1;

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S70782; AAB31163.2;
D29952; BAA06222.1;
                                                                       Genew; HGNC:280; ADRAID.
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                                                           JH0447;
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-95114877; PubMed-7815325; Schwinn D.A., Wollson K.H., Schwinn D.A., Johnston G.I., Page S.O., Wosley M.J., Wilson K.H., Worman N.P., Campbell S., Fidock M.D., Furness L.M., Parry-Smith D.J., Peter B., Bailey D.S.; Cloning and pharmacological characterization of human alpha-1 adrenergic receptors: sequence corrections and direct comparison with other species homologues."
J. Pharmacol. Exp. Ther. 272:134-142(1995).
                                                                                                                                                                                                                                          Bruno J.F., Whittaker J., Song J., Berelowitz M.; "Molecular cloning and sequencing of a CDNA encoding a human alpha lA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-94296402; PubMed-8024574;
Weinberg D.H., Trivedi P., Tan C.P., Mitra S., Perkins-Barrow A.,
Borkowski D., Strader C.D., Bayne M.;
"Cloning, expression and characterization of human alpha adrenergic
receptors alpha la, alpha lb and alpha lc.";
                                                                                                                                                                                                                                                                                                                                                                                                                      οţ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THROUGH THE INPLUX OF EXTRACELLULAR CALCIUM.
-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                              Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                    "The alpha 1-adrenergic receptor that mediates smooth muscle contraction in human prostate has the pharmacological properties the cloned human alpha 1c subtype.";
MOI. Pharmacol. 45:703-708(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minneman K.P., Murphy T.J.;
"Cloning of the human alpha 1d-adrenergic receptor and inducible expression of three human subtypes in SK-N-MC cells.";
Mol. Pharmacol. 47:977-985(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Placenta, and Prostate;
MEDLINE-95265059; PubMed-7746284;
Esbenshade T.A., Hirasawa A., Tsujimoto G., Tanaka T., Yano J.,
                                                     01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Alpha-1D adrenergic receptor (Alpha 1D-adrenoceptor) (Alpha-1A
                                                                                                                                                                                                                                                                                                                              TISSUE-#ippocampus;
MEDLINE-94239386; PubMed-8183249;
Forray C., Bard J.A., Wetzel J.M., Chiu G., Shapiro E., Tang
Lepor H., Hartig P.R., Welnshank R.L., Branchek T.A.,
                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         eceptors alpha la, alpha 1b and alpha 1c.";
Lochem. Blophys: Res. Commun. 201:1296-1304(1994).
                                                                                                                                                                                                                                                                                   3iochem. Biophys. Res. Commun. 179:1485-1490(1991).
              572 AA.
                PRT;
                                                                                                                                                                                                               TISSUE-H1ppocampus;
MEDLINE-92028892; PubMed-1656955;
                                            Created)
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              STANDARD;
                                                                                                 adrenergic receptor).
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                                                                                                                ADRAID OR ADRAIA.
                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                       uchowski C.;
                                         01-MAY-1992
              A1AD_HUMAN
                            P2510(
Alad_Homan
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S -> G (IN REF. 4).
KPPSAFREWRLLGPFRRPTTOLRAKVSSLSHKIRAGGAOR
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VNG -> MAAALRSVMMAGYLSEWRTPTYRSTEMVQRLRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AEAACAQRSEVEAVSLGVPHEVAEGATCQAYELADYSNLR
ETDI -> SHPAPSASGGCWGRSGDPRPSCAPKSPACRTR
                                                                                                                                                                                                                                                                                                                                                                    MTFRDLLSVSFEGPRPDSSAGGSSAGGGGGSAGGAAPSEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
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         3
                   PIGETLY, Thun 1: 1.

PRINTS: PRO0021; CPCRRHODOPSN.

PROSITE: PS00237; CPCRRHODOPSN.

PROSITE: PS00237; CPROTEIN.RECEP_FL_1; 1.

PROSITE: PS50262; C_PROTEIN_RECEP_FL_2; 1.

G_PROTEIN COUPLED receptor; Transmembrane; Glycoprotein;

G_PROTEIN COUPLED FOR PROSPHORYLATION; Lipoprotein; Palmitate.

Multigene family; Phosphorylation; Lipoprotein; Palmitate.

95
                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL).
                                                                                                                                                             2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -> P (IN REF. 4).
EBEB134CF20A4988 CRC64;
                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
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POLY-ARG.
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Mismatches:
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(Rel. 39, Last sequence update)
(Rel. 41, Last annotation update)
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Matches:
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               IPR000276; GPCR_Rhodpsn.
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RV2850c OR MT2916 OR MTCY24Al.07.
Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  522 1
60462 MW;
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100.00%
1.16%
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8.00
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159
169
192
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572 AA;
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Best Local Similarity:
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170
193
214
252
252
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374
381
406
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YS50_MYCTU
YS50_MYCTU
YS50_MYCTU
104219;
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15-JUN-2002
                InterPro;
                                                                                                                                              DOMAIN
TRANSMEM
DOMAIN
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TRANSMEM
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Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus
                   NCBI_TaxID=1351;
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Q63801;
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                                                                                                                                                                                               SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Raff D., Hickey E.,
Peterson J., DeBoy R., Dodson R., Gwinolaeva M.D., Salzberg S.L.,
Kolonay J.F., Nelson W.C., Weldman J., Khouri H., Gill J., Mikula A.,
Delcher A., Utterback T., Weldman J., Khouri H., Gill J., Mikula A.,
                     Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.Y., Eiglaneier K., Gas S., Barry C.E. Ili, Frekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Peltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Woule S., Murphy L., Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitchead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."
                                                                                                                                                                                                                                                                                                                                        01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Autolysin precursor (EC 3.2.1.-) (Peptidoglycan hydrolase)
(Beta-glycosidase).
Enterococcus faecalis (Streptococcus faecalis).
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Matches:
Conservative:
Mismatches:
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InterPro; IPR000523; Mg_chelatse_chII.
InterPro; IPR002035; VWR_A.
Pfam; PF01078; Mg_chelatase; 1.
SWART; SM00327; VWR; 1.
PROSITE; PS50234; VWRA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCACAGGGTCCACTGAAACGGGG 2001
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         MEDLINE-98295987; PubMed-9634230;
                                                                                                                                                                                                                                                                                                                                                                                                                     frameshift in position 19.
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100.00%
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                                                                                                                                                                                  Nature 393:537-544(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein;
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Best Local Similarity:
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P37710;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
        MEDLINE-91368349; PubMed-1679432;
Beliveau C., Potvin C., Trudel J., Asselin A., Bellemare G.;
Beliveau C., Potvin C., Trudel J., Asselin A., Bellemare G.;
Beliveau C., Potvin C., Trudel J., Asselin A., Bellemare G.;
Cloning, sequencing, and expression in Escherichia coli of a Streptococcus faccalis autolysin.";
J. Bacteriol, 173:5619-5623 (1991).
I. Subcritol, HYDROLYZES THE CELL WALL OF E.FAECALIS AND
M.LYSODERTATIONS. NAY PLAY AN IMPORTANT ROLE IN CELL WALL GROWTH
AND CELL SEPARATION:
Secreted (Probable).
--- DOMAIN: LYSM REPEATS ARE THOUGHT TO BE INVOLVED IN PEPTIDOGLYCAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
17-JUN-2002 (Rel. 41, Last annotation update)
17-JUN-2002 (TAFII80) (P80)
17-JUN-1809 (TAFII80) (P80)
17-JUN-1809 (TAFII80) (P80)
                                                                                                                                                                                                                                                                                                                                   -1- SIMILARITY: BELONGS TO FAMILY 73 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            enzyme; Cell wall;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LYSM 5.
3458268C6C1A4A33 CRC64;
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Indels:
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Matches:
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Cell division; Septation; Repeat; Signal..
SIGNAL 1 53 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-824-647-16 (1-2095) x ALYS_ENTFA (1-671)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTOLYSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LYSM 1.
LYSM 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LYSM 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         383 TCCAGTGCCCTGATAGTCAGTTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002901; Amidase_4.
InterPro; IPR002482; LysM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70442 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01476; LysM; 5.
Pfam; PF01832; Amidase_4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M58002; AAA67325.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.9
8.00
100.00%
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1.15%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00047; LYZ2; 1. SMART; SM00257; LYSM; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A38109; A38109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              671 AA;
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity:
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                                                                                                  -I- FUNCTION: TFILD IS A MULTIMERIC PROTEIN COMPLEX THAT PLAYS A CENTRAL FOLD.

CENTRAL FOLD IN MEDIATING PROMOTER RESPONSES TO VARIOUS ACTIVATORS AND REPRESSORS.

INTERACTS WITH TAFIL 40.

-I- SUBDUIT: FIPID IS COMPOSED OF TATA BINDING PROTEIN (TBP) AND A NUMBER OF TBP-ASSOCIATED FACTORS (TAFS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-20057165; PubMed-10591208; Brusklewich R., Beare D.M., Clamp M., Smink L.J., Ainscough R., Ainelda J.P., Babage A.K., Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P., Balkey S.E., Bridgeman A.M., Buck D., Burgess J., Burtli W.D., Button J., Carder C., Carter N.P., Chen Y., Clark G., Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R., Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J.D. Dawson E., Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G., Bvans K.L., Fey J.M., Fleming K., French L., Garner A.A., Gilbert J.G., R., Goward M.E., Graffen D.V., Criffiths M.N.D., Hall C., Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,
                      TISSUE-Testis;
MEDLINE-95394378; PubMed-7665101;
Kida S., Umehara T., Horikoshi M.;
"Three distinct regions in a rat TFIID subunit containing histone H4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ROXN_HUMAN STANDARD, PRT; 993 AA.
09UGR2; Q9UFW9; Q9UGQ9; Q9UGR0; Q9UGR1; Q9UK03; Q9H8B6;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ROIN-2004 (Rel. 41, Last annotation update)
ROIN-2004 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                    Transcription regulation; Nuclear protein.
SEQUENCE 678 AA; 72713 MW; 92D7225E3B7CC171 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                              SIMILARITY: BELONGS TO THE TAFZE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels:
                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-824-647-16 (1-2095) x T2D5_RAT (1-678)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1053 GGCCCCAGCTCACCTCAGCCTGCC 1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            670 GlyProSerSerProGlnProAla 677
                                                                                                                                                                                                                                                                                                                                               InterPro; IPR004822; Histone_core.
InterPro; IPR004823; TFIID_TAF.
Pfam; PF02969; TAF; 1.
                                                                                                                                                                                                                                                                                                                               EMBL; D49446; BAA08435.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.00%
100.00%
1.15%
                                                                           homology.";
Gene 161:303-304(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ROXN_HUMAN
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RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
RA Martyn I.D., Mashrepil-Mohamadi M., Matthwa L.H., Mordinnore B.J.,
RACLAY J., McLaren S., McMurray A.A., Milne S.A., Mortinnore B.J.,
RA Colai C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
RA Scott C.E., Sehra H.K., Stuce C.D., Samiley S., Smith M.L.,
RA Vandin M., Wall M., Walles Y. W.N., Willey D.L.,
Williams L., Williams S.A., Williamson H., Winner T.E., Wilming L.,
Williams L., Milliams S.A., Williamson H., Wilmer T.E., Wilming L.,
Williams L., Rawsaki K., Sasaki T., Asakwas S., Roders J., Shimizu N.,
Rhinchina S., Kawasaki K., Sasaki T., Asakwas S., Roders J.,
Shintani A., Shibuya K., Yoshizaki Y., Asakwas S., Roder J.,
Shintani A., Shibuya K., Yoshizaki Y., Asakwas S., Lewis S., Lai S., Lin S.-P., Loh P., Walaj E., Nguyen T., Pan H.,
Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Da A., Do T.,
RA Dorman A., Fang F., Pu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA Cordes M., Du Z., Frilton L., Goela D., Graves T., Hawkins J.,
Rhos S., Gian Y., Ray L., Wollidmann P., Pepin K., Wilson J.,
Rhos Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R.,
Rhoter P., Walker C., Wamsley A., Wohldmann P., Pepin K., Wilson J.,
Rhoter P., Walker C., Wornew B.E., Edelmann L.,
Bmanuel B.S., Shaikh T., Kurahashi H., Saitta S., Budarf M.L.,
Bmanuel B.S., Shaikh T., Kurahashi H., Saitta S., Budarf M.L.,
Bmanuel B.S., Shaikh T., Kurahashi H., Suon P., Peyrard M., Kedra D.,
Sercoussi E., Fransson I., Tapia I., Burder C.E., O'Brien K.,
Wilkinson P., Bodenteich A., Hartman Chram P., R.,
Wilkinson P., Bodenteich A., Hartman Chram P.,
Wilki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kikuno R., Nagase T., Ishikawa K.-I., Hirosawa M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Preddiction of the coding sequences of unidentified human genes. XIV. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- SUBCELLULAR LOCATION: Nuclear (Probable).
-i- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be produced by alternative splicing.
-i- SIMILARITY: CONTAINS 2 TPR REPEATS.
-i- SIMILARITY: CONTAINS 1 C2H2-TYPE ZINC FINGER.
-i- SIMILARITY: CONTAINS 4 C3H1-TYPE ZINC FINGERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Res. 6:197-205(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The DNA sequence of human chromosome 22.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 38-993 FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-780 FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-99397452; PubMed-10470851;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 402:489-495(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGF-LIKE 15.
EGF-LIKE 16 (N-TERMINAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGF-LIKE 11 (INCOMPLETE) EGF-LIKE 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAMININ HOTERMINE (DOMAIN VI).
LAMININ NOTERMINE (DOMAIN VI).
LAMININ BGF-LIKE 1.
LAMININ BGF-LIKE 2.
LAMININ BGF-LIKE 4.
LAMININ BGF-LIKE 5.
LAMININ BGF-LIKE 6.
LAMININ BGF-LIKE 7.
LAMININ BGF-LIKE 7.
LAMININ BGF-LIKE 10.
LAMININ BGF-LIKE 10.
LAMININ BGF-LIKE 11.
LAMININ BGF-LIKE 11.
LAMININ BGF-LIKE 11.
LAMININ BGF-LIKE 11.
LAMININ BGF-LIKE 12.
LAMININ BGF-LIKE 14.
LAMININ BGF-LIKE 14.
LAMININ BGF-LIKE 14.
LAMININ BGF-LIKE 14.
LAMININ BGF-LIKE 15.
LAMININ BGF-LIKE 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN IV.
EGF-LIKE 16 (C-TERMINAL)
EGF-LIKE 17.
SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV. SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAMININ G-LIKE 1.
LAMININ G-LIKE 2.
LAMININ G-LIKE 3.
LAMININ G-LIKE 4.
LAMININ G-LIKE 5.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAMININ EGF-LIKE
LAMININ EGF-LIKE
LAMININ EGF-LIKE
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                                                                                                                                                                                                                                                                             InterPro; IPR000561; EGF-1ike.
InterPro; IPR001886; LamWT.
InterPro; IPR0001886; LamWT.
InterPro; IPR000244; Laminin_B.
InterPro; IPR001949; Laminin_G.
Pfam; PR00052; Laminin_B; 1.
Pfam; PR00053; laminin_B; 1.
Pfam; PR00054; laminin_G; 5.
Pfam; PR00055; laminin_G; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0011; EGFLAMININ.
ProDom; PD002082; LamNT; 1.
ProDom; PD003031; LamNinin_B; 1
SWART; SW00180; EGF_Lam; 21.
SWART; SW00281; LamB; 1.
SWART; SW00282; LamG; 5.
SWART; SW00186; LamK; 1.
PROSITE; PS00022; EGF_1; 19.
PROSITE; PS01186; EGF_2; 4
                                                                                                                                                                                                                      EMBL; Z70286; CAA94293.1; -. HSSP; P02468; 1KLO.
                                                                                                                                                                                                                                                          MormPep; K08C7.3; CE06136.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS01248;
PROSITE; PS50025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           461
506
554
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2896
3072
3310
3488
322
334
334
359
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      REMBL; AL035659; CAB62495.1; -.

REMBL; AL035659; CAB62495.1; -.

REMBL; AL035659; AAF05541.1; -.

REMBL; AR108549; BAA62963.1; -.

REMBL; AR02849; BAA62963.1; -.

REMBL; AR02849; BAA62963.1; -.

REMBL; AR02849; BAA62963.1; -.

REMBL; AR028954; BAA62963.1; -.

REMBL; AR028954; BAA62963.1; --

REMBL; AR00955; ZAFCCH2.

DR Pfam; PRO0065; ZAFCCH2.1

REMBL; RAN0355; ZAFCCH3.1

DR Pfam; PRO0065; ZAFCCH3.1

REMART; SAN00355; ZAFCCH3.1

REMBL; RANOSSE, ZAFCCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MISSING (IN ISOFORM 2).

NL -> LE (IN REF. 4).

R -> K (IN REF. 2).

GTSNGLGSIDDIET -> VGSGLNQPVSVIPL (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Berks M.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 1 LAMININ N-TEEMINAL DOMAIN (DOMAIN VI).
-!- SIMILARITY: CONTAINS 21.5 LAMININ EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3).

G -> A (IN REF. 2).

G -> V (IN REF. 2).

S -> F (IN REF. 1; CAB62495 AND 2).

WW; B81E9E67772FFEIB CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Laminin-like protein KO8C7.3 precursor.
KO8C7.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPR 1.
TPR 2.
C3H1-TYPE 1.
C3H1-TYPE 2.
C3H1-TYPE 3.
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386
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993 AA;
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Query Match:
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Q21313;
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LML2_CAEEL
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(POTENTIAL)	3672 8 8 0 0 0 0	AA. te) date) 34; Somatostatin-14]. Vertebrata; Hyperoartia; romyzon. , Youson J.H., lant somatostatin-14 and two ues from lamprey (Petromyzon RELEASE OF SOMATOTROPIN. TIN FAMILY.
BY SIMILARTTY. N-LINKED (GLCNAC N-LINKE	Length: Matches: Conservativ Mismatches: Indels: Gaps: (1-3672) 1119	RT; 37 AA. ance update) attion update tostatin-34; costatin-34; dott W.M., You lidae; Petromy idae;
2117 2129 121 121 140 249 249 249 249 249 351 477 477 477 5511 5511 510 510 1014 1014 1014 11756 1756 11756 1756 11868 1868 1986 1986 2002 2002 2002 2002 2159 215 2231 2231 2421 2421 2421 2421 2431 2431 2431 2431 2431 2431 2441 2441 2441 2441 2451 2451 2471 2471 2471 247	es: 28.3 8.00 s.tity: 100.00\$ 1.16\$ 1.16\$ 16 (1-2095) x LML2_CAEEL GTATCGGAGGAGGACACCTGCTG	DARD; 8, Creat 8, Last 0, Last 0, Last Chordat Chordat Petrom betrom 0 34 15809-15 0STATIN ATION: 1 SOMACT 1 SO
DISULFID CARBOHYD CAR	nment Scor . No.: e: ent Simila ent Simila y Match: 9-824-647- 1142	ULT 37 PETMA SMS_PETMA SMS_PETMA P21779; 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 16-OCT-20 Somatosta Petromyzc Petromyzc Petromyzc NCBL [1] LEXATYOTA FETMATORY [1] LOUINE-6 MEDLINE-6 FISOLATIO Telated s marinus). J. Blol1 FUNCT -1 SIMCI -1 SIMCI PIR; A320 PIR; A320 PIR; A320
255555555555555555555555555555555555555	Aligum Pred. Score: Percen Best L Query DB: US-09- QY	RESULT OF THE PARTY OF THE PART

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                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation
                        Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
                                                                          MEDLINE-90094217; PubMed-2152899; Gray J.X., Djordjevic M.A., Rolfe B.G.; Gray J.X., Djordjevic M.A., Rolfe B.G.; Two genes that regulate exopolysaccharide production in Rhizobium sp. strain NGR234: DNA Sequences and resultant phenotypes."; J. Bacteriol. 172:193-203(1990).
                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE010337; AAM01633.1; -.
PROSITE; PS01168; RIBOSOMAL_S27E; 1.
Ribosomal protein; Zinc-finger; Metal-binding; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhizobium sp. (strain NGR234).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                       ZN_FING 28 50 C4-TYPE.
SEQUENCE 73 AA; 8281 MW; PE715056D29C0E8B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-JAN-2002 (Rel. 41, Last annotation update)
Exopolysaccharide production repressor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NODGLATION ABILITY (NOD).
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OR RPS27A OR: MK0418
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             Methanopyrus kandleri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Best Local Similarity:
                                           Methanopyrus.
NCBI_TaxID=2320;
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P14185;
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 RPS27E
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                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ranes-Goldberg M.G., Hori T., Mohan-Peterson S., Spits H.; "Identification of human pre-T/NK cell-associated genes."; J. Immunol. 151:5810-5821(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L17330; AAA16782.1; -.
SEQUENCE 57 AA; 6068 MW; CD41EAFFD2161857 CRC64;
                                                        5918153B2775AC4D CRC64;
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Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
Indels:
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16-CCT-2001 (Rel. 40, Last sequence update)
15-JWR-2002 (Rel. 41, Last annotation update)
15-TWR cell associated protein 6H9A.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
30S ribosomal protein 527e.
                                SOMATOSTATIN-14.
                                                                                                                                                                                                                                                                                                               57 AA.
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                  SOMATOSTATIN-34
  Cleavage on pair of basic residues; Hormone. PEPTIDE 4 37
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                  37
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4039 MW;
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                              24
26
37 AA;
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Best Local Similarity:
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Pred. No.:
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Q8TY87;
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Q13653;
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                                             DISULFID
SEQUENCE
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                                 PEPTIDE
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RS27_METKA
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US-09-824-647-16 (1-2095) x SSIC_STRHY (1-111)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-96176850; PubMed-8597568; Terabe M., Miura K.-I.; Terabe M., Kofilma S., Taquchi S., Momose H., Miura K.-I.; New subtilisin-trypsin inhibitors produced by Streptomyces: primary structures and their relationship to other proteinase inhibitors from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: BELONGS TO THE SERINE PROFEASE INHIBITORS SSI FAMILY.
HSSP; PO1006; 3SSI.
InterPro; IPR000691; Strep_subt_inhib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochim. Biophys. Acta 1292:233-240(1996).
-!- FUNCTION: STROM INHIBITORY ACTIVITY TOWARD SUBTILISIN BPN' AND
TO A LESSER EXTENT, TO TRYPSIN.
-!- SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Streptomyclneae; Streptomyces.
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                                                                                                                                                                                                                                        Exopolysaccharide synthesis; Nodulation; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09R641;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Subtilisin inhibitor-like protein-12 (SIL-12) (SIL12).
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PRINTS; PR00294; SSBTLAINHBPR.
ProDom; PD004028; Strep_subt_inhib; 1.
PROSITE; PS00999; SSI; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29 AlaSerThrAlaValGlnThr 35
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100.00%
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                                                                                                                                                                                                          EMBL; X16704; CAA34675.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                         25
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                         96 AA;
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RA Amanatides P. G., Scherer S. E., 101 P. W., Hoskins R. A., Galle R. F.,

RA Amanatides P. G., Scherer S. E., 11 P. W., Hoskins R. A., Galle R. F.,

RA Amanatides P. G., Scherer S. E., 11 P. W., Hoskins R. A., Galle R. F.,

RA Amanatides P. G., Scherer S. E., 11 P. W., Hoskins R. A., Galle R. F.,

Burdon R. C., Paxter E. G., Helf G., Nelson C. R., Miklos G. L. G.,

RA Brandon R.C., Baxter E. G., Helf G., Nelson C. R., Miklos G. L. G.,

RA Abrill J. F., Agbayani A., Bardell M. D., Bolshakov S.,

RA Ballew R. M., Basu M., Bardadle J., Brotater P., Borcker B. B.,

Borkova D., Botchan M. R., Buuck J., Brokstein P., Brottier P.,

RA Borkova D., Botchan M. R., Buuker H., Cadleu E., Center A., Chandra I.,

RA Calley B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S. M.,

RA Callery J. M., Cawley S., Dahlke C., Davenport L. B., Davies P.,

RA Changon K., Doup L. E., Downes M., Dugan Rocha S., Plukov B. C.,

RA Burtis K.J., Evangelista C.C., Ferraz C., Ferriera S., Plakschman W.,

RA Googn K., Doup L. E., Downes M., Dugan Rocha S., Plakschman W.,

RA Harris M.L., Harvey D., Halman T. J., Hernandez J. R., Houck J.,

RA Harris M.L., Harvey D., Halman T. J., Hernandez J. R., Houck J.,

RA Harris M.L., Harvey D., Halman T. J., Hernandez J. R., Molte J. L.,

RA Harris M.L., Mattel B., McInton R., Krafft C., Kravitz S., Kulp D., Lai Z.,

Liu X., Mattel B., McInton R., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

Ralazdolo M., Pittama G.S., Pan S., Pollard J., Walley R., Murphy L., Mazny D.M., Nelson D.K.,

Ralazdolo M., Pittama G.S., Pan S., Pollard J., Walley R., Shie B.C., Siden-Klamos I., Simpson M., Strong R., Shie B.C., Siden-Klamos I., Simpson M., Strong R., Walleshenbard S., Ranger R., Yeller E., Spradling A.C., Stapheton M., Strong R., Walleshenbard S., Worley K.C., Wu D., Yeller S.,

Ra Milliams S.M., Woodage T., Worley R., Waller E., Shap G., Shan R., Shan R., Reiner R., Worley 
                                                                                                                                                                                                                                                                     LCP3 OR CG2043.

Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Mandibulàta; Pancrustacea; Hexapoda;

Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID-7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'Cuticle protein genes of Drosophila: structure, organization and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- FUNCTION: COMPONENT OF THE CUTICLE OF THE LARVA OF FRUIT FLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Snyder M., Hunkapiller M., Yuen D., Silvert D., Fristrom J.,
                                                                                                                                CLP3_DROME, STANDARD; PRT; 112 AA. P07189; Q9V4T1; 01-APR-1988; (Rel. 07, Created) 15-APR-1988 (Rel. 07, Last sequence update) 15-JUN-2002; (Rel. 41, Last annotation update) Larval cutifie protein III precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-Oregon-R, and Canton-S; TISSUE-Larva;
MEDLINE-83103095; PubMed-6817923;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         evolution of four clustered genes.";
550 ACACCCACGGGCACCCACCCC 570
                          4 ThrProThrGlyThrHisPro 40
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                                                                                     RESULT 42
CLP3_DROME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-20504483; PubMed=11016950; Merquist B., Pan M., MEDLINE-20504483; PubMed=11016950; Merdist B., Pan M., Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M., Shukla H.D., Lasky S.R., Baliga N.S.; Thorsson V., Sbrogna J., Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A., Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W., Maddocks D.G., Jablonski P.E., Frebs M.P., Angevine C.M., Dale H., Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung R.-H., Bhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S., "Genome sequence of Halobacterium species NRC-1."; Proc. Natl. Acad. Sci. US.A. 97:12176-12181(2000).
                                                                                                                                                                                                                                                                                                                               LARVAL CUTICLE PROTEIN III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
                                                                                                                                                                                                                                                                                                                                                    PRO-RICH.
2C6AC731B77291A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-824-647-16 (1-2095) x CLP3_DROME (1-112)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
                                                                                                                                                                                                                    RlyBase; FBgn0002534; Lcp3.
InterPro; IPR000618; Insect_cuticle.
Pfam; PF00379; Chitin bind 4; 1.
PROSITE; PS00233; CUTICLE; 1.
                                                                                                                                                                                                                                                                                         Structural protein; Cuticle; Signal. SIGNAL 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1130 CCTCCTCCGATACCTGCTGCC 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Halobacterium sp. (strain NRC-1). Plasmid pNRC200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91 ProProProlleProAlaAla 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Halobacteriaceae; Halobacterium.
NCBI_TaxID-64091;
                                                                                                                                                              EMBL; V00203; CAA23489.1; -.
EMBL; AE003837; AAF59094.1; -.
PIR; C25299; C25299.
                                                                                                                                                                                                                                                                                                                                                                     112 AA; 11857 MW;
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100.00%
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GVPI2 OR VNG6233G.
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                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match:
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GVI2_HALN1
                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.:
                                                                                                                                                                                                                                                                                                                                     CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Huang 2., Depoortere I., De Clercq P., Peeters T.; "Sequence and characterization of cDNA encoding the motilin precursor from chicken, dog, cow and horse. Evidence of mosaic evolution in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene 240:217-226(1999).
-i- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE REGULATION OF INTERDIGESTIVE GASTROINTESTINAL MOTILITY AND INDIRECTLY CAUSES RHYTHAIC CONTRACTION OF DUODENAL AND COLONIC SMOOTH MUSCLE (BY
                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus (Bovine).
Skaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39) Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last amontation update)
Motilin precursor [Contains: Motilin; Motilin associated peptide (MAP)].
                                                                                 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRC64;
                proteome.
DEBFFF8033A0473E CRC64;
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                                                                      1113
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                    Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                       115 AA.
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MOTILIN.
                                                                      Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch)
                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rISSUE=Duodenal mucosa;
MEDLINE=20033565; PubMed=10564829;
                                                                                                                                                                                                         603
                                                                                                                                                                                                      e; Plasmid; Complete
113 AA; 12526 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 AA; 13055 MW;
EMBL; AE005156; AAG20889.1;
Gas vesicle; Plasmid; Comple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  458
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Best Local Similarity:
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Hutt B., Hont S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., McDonay P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Nell S., Pearson D., Quail M.A., Rablnowitsch E., Selton J., Simmonds M., Squares R., Seevens K., Starp S., Stevens R., Stelton J., Simmonds M., Squares R., Stevens R., Stelton J., Simmonds M., Squares R., Stevens R., Stelton J., Volckaert G., Aert R., Robben J., Grymonrez B., Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., A. Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Danga R.R., Cruzado L., Jimenez J., Sanchez M., Gel Rey F., Benito J., Sanchez M., Sanchez M., Gel Rey F., Benito J., Sanchez M., Gel Rey F., Benito J., Sanchez M., Sanchez M., Sanchez M., Sanchez M., Gel Rey F., Benito J., Sanchez M., Sanchez M., Gel Rey F., Benito J., Sanchez M., Sanche
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ., Churcher C.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Ste
Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman
Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BOC842741F30326D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                                                                                                                                                                 01-027-1996 (Rel. 34, Created)
01-027-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Very hypothetical protein C26F1.05 in chromosome I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                       115 AA.
                                                                                                                                                                                                                                                                                                                                                                                                               Schizosaccharomyces pombe (Fission yeast).
US-09-824-647-16 (1-2095) x MOTI_BOVIN (1-115)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
                                                                                                                                                                                                         PRT;
                                                     1679 GCCACTGCTGTCCTGCTGGCT 1699
                                                                                    6 AlaThrAlaValLeuLeuAla 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-21848401; PubMed-11859360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ll protein.
115 AA; 13477 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z73100; CAA97362.1; -.
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                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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010493:
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                                                                                                                                                                                             7DG5_SCHPO
                                                                                                                                                                 RESULT 45
                                                                                                        QQ
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US-09-824-647-16 (1-2095) x YDG5_SCHPO (1-115)

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Q26036 trypanosoma
Q9b134 cyprinella
Q9b134 cyprinella
Q9d597 mus musculu
Q3120 homo sapien
Q07154 mycobacteri
Q915p6 pseudomonas
Q9x549 corynebacte
Q916w2 hepatitis c
Q916w1 hepatitis s
Q916w1 hepatitis c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9rrk2 deinococcus
O75608 homo sapien
O77821 oryctolagus
P70470 rattus norv
P97823 m lphosphol
Q9v8a8 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9rz01 deinococcus
Q9at16 zea mays (m
Q9pa28 xylella fas
O69819 streptomyce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8qs62 chimpanzee
Q911t8 streptomyce
          Q9x402 methylosulf
Q8vuf4 azoarm
                                                                               Q8y2x4 ralstonia s
P74015 synechocyst
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Q39263 arabidopsis
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musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ogbux4 homo sapien
Oguqf9 homo sapien
O77820 oryctolagus
                                                                                                                                           trypanosoma
                                                                                                                                                                                    trypanosoma
                                                                                                                                                               Q98ke0 rhizobium
                                                                                                                        drosophila
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TISSGE-OVARIAN CARCINOMA;

TISSGE-OVARIAN CARCINOMA;

Nishikawa T., Otsuki T., Sudon H., Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S., Watanbashi M., Chiba Y., Marakami K., Ishili S., Kawai Y., Saito K., Yamanoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Inaniomiya K., Iwayanagi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordăta; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                Q26763
Q26036
Q9b134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEDO human cDNA sequencing project.";
submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AK023348; BAB14535.1;
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Last annotation update)
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08QQM8
084305
09PK90
08XX13
08QS62
09L1T8
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P97823
Q9V8A8
Q9RZ01
Q9ATL6
Q9PA28
O69819
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Q8Y2X4
P74015
Q18414
Q26835
Q96KE0
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026036
029B134
09D5G7
043202
007154
0915P6
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O77820
Q9RRK2
O75608
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039263
09C8D2
08RUU4
099MA1
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                                                                                                633
1191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted
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Q9H8S1
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-QP-C902_1/R05FO_5800_1/R059824647/xunat_07072003_154718_26035/app_query.fasta_1.2247
-QP-C902_1/R05FO_5800_1/R059824647/xunat_07072003_154718_26035/app_query.fasta_1.2247
-DB-SPREMBL_21 -OFWT-fastan -SUFFIX-sept -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-blits -START=1 -END=-1 -MATRIX=01190 -TRANS=human40.cd1
-LIST=45 -DGCALIGH=200 -THR_SCORES=04114y -THR_MINF1 - ALIGH=45 -MODE=LOCAL
-OGTFMT-pct -NORM-ext -HEARSIZE=500 -MINIX=N-0 -MAXIEN=200000000
-USER-US09824647_CGCN_1 1_231_erunat_07072003_154718_26035 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NRG_SCORES=0 -WART -DSPBLOCK=100 -LONGLOG
-FGAPOP=60 -VGAPORT=60 -DELLOP=6 -DELEXT=7
-YGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELLOP=6 -DELEXT=7
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                                                                                                                                 7, 2003, 15:47:40 ; Search time 159.5 Seconds (without alignments) 5412.774 Million cell updates/sec
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                                                                                                                                                                                                                                                                1 cgcaggcagaccatgtggac......ataaagtttgtcactttctt 2095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1343044
                 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

    protein search, using frame_plus_n2p model

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                                                                                                                                                                                                                                                                                                                                                                                                                               seqs, 206047115 residues
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sp_human:*
sp_invertebrate:*
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sp_phage:*
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sp_bacteria:*
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sp_rodent:*
sp_virus:*
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Match Length DB
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Xgapop
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Title:

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GCTGTGTGCTGTGAGGACCACATACACTGCTGTCCCGCGGGGTTTACGTGTGACACGCAG 1005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alzawa M., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1186 CCAGAGGCTGTCTGCTGCTCGGACCACCAGCACTGCTGCCCCCAG 1230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TTEMBLE). 17, Last Sequence update)
01-JUN-2002 (TTEMBLE). 11, Last annotation update)
Adult male kidney CDNA, RIKEN full-length enriched library,
clone:0610012H06, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000118; Granulin.
InterPro; IPR001211; PhospholipaseA2.
Pam; PR00396; granulin; 4.
SWART; SW00277; GRAN; 4.
PROSITE; PS00799; GRANULINS; UNKNOWN, 4.
PROSITE; PS01198; PAZ, HI35; UNKNOWN, 1.
SEQUENCE 413 AA; 44132 WW; 0E3767A44BE314EC CRC64;
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155
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Matches:
Conservative:
Mismatches:
Indels:
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MEDLINE-21085660; PubMed-11217851;
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155.00
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Best Local Similarity:
                                                                                                         Alignment Scores:
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1396 GGGAGCTGGCCTGCTGCCGGTTGCCCCATGCTGTGTGCTGCGAGGATCGCCAGCACTGC 1455
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Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schrill L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Paruno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hoffmann M., Hume D.A., Kaniya M., Lee N.B., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerfä P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Willming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     460 GlySerTrpAlaCysCysGlnLeuProHisAlaValCysCysGluAspArgGlnHisCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDINE-93266526; PubMed-8496151;

AEDLINE-93266526; PubMed-8496151;

Zhou J., Gao G., Crabb J.W., Serrero G.;

Purification of an autocrime growth factor homologous with mouse epithelin precursor from a highly tumorigenic cell line.";

J. Biol. Chem. 268:10863-10869(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_raxID=10095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAY-2000 (TrEMBLrel. 13, Last annotation update)
PC cell-derived growth factor, PCDGF-EPITHELIN precursor homolog
                                                                                                                                                                                                 Hayashizaki Y.;
*Punctional funotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                         EMEL; AKO1874; BAB31384.1; -
EMEL; AKO1874; BAB31384.1; -
MGI; 95832; Grn.
InterPro; IPR000118; Granulin.
InterPro; IPR0001211; PhospholipaseA2.
Pfam; PF00396; granulin; 7.
PROSITE; SM00277; GRAN, 7.
PROSITE; PS00799; GRANULINS; 7.
PROSITE; PS00118; PA2_HIS; UNKNOWN_1.
SEQUENCE 589 AA; 63405 MW; IDE8229C413CA292 CRC64;
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Indels:
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Matches:
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Alignment Scores:
Pred. No.:
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Kenna E.M., Murrell J.C.;
"Molecular analysis of a novel methanesulfonic acid monooxygenase from
the methylotroph Methylosulfonomonas methylovra.";
J. Bacteriol. 181:2244-2251(1999).
BMBL; AF091716; AAD26617.1;
NON TER 266 266
SEQUENCE 266 AA; 29281 MW; 2AFAEDC02B575010 CRC64;
                                                                                                                                                05X402;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
Putative ABC transporter membrane-associated protein (Fragment).
                                                                                                                                                                                                                                           Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Methylosulfonomonas.
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; A4128529; CAD21637.1; -
InterPro; IPR002085; Adh.zu_family.
InterPro; IPR0000345; CytC_heme_bind.
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PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
SEQUENCE 355 AA; 38211 MW; 5E1D930131F800A6 CRC64;
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01-WAR-2002 (TTEMBLrel. 20, Last sequence update)
01-JUN-2002 (TTEMBLrel. 21, Last annotation update)
6-hydroxycyclohex-1-ene-1-carboxyl-CoA dehydrogenase.
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Matches:
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                                  US-09-824-647-16 (1-2095) x Q9QWB4 (1-51)
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100.00%
1.30%
1.30%
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Best Local Similarity:
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Query Match:
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STRAIN-GMI1000;

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SATION-STATE A. STATE A. GOUZY J., Mangenot S., Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottler P., Camus J.C., Cattolico L., Arlat M., Chisne N., Claudel-Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin M., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.;

"Genome sequence of the plant pathogen Ralstonia solanacearum.";
Nature 415:497-502(2002).
                                                                                      . Si
                                                                                                                                                                                                                                                                                                                                                                                                                                  Ralstonia solanacearum (Pseudomonas solanacearum).
Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
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Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
NCBL_TaxID=1148;
355
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNY-2002 (TrEMBLrel. 21, Last annotation update)
Putative transporter transmembrane protein.
RSC0207 OR RS00639.
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Q8Y2X4;
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                                                           Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura T., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Miraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
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Pterygota; Neoptea; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                    Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
DNA Res. 3:109-136(1996).
INDIARATY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER REGULARORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS.
I-SIMILARITY: TO PROKARYOTE SENSORY TRANSDUCTION PROTEINS.
ISBMB: D10911; BAA18086.1;
HSSP; P10957; IRML.
                                                                                                                                                                                                                      *Sequence analysis of the genome of the unicellular cyanobacterium
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InterPro; IPR004358; Bact_sens_pr_C.
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MEDLINE-98037748; PubMed-9367989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00344; BCTRLSENSOR.
ProDom; PD000039; Response_reg; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro; IPR003018; GAF.
Interpro; IPR003661; His_kina.
Interpro; IPR004359; HIS_Kin sig.
Interpro; IPR001789; Response_reg
   SEQUENCE FROM N.A.
MEDLINE-97061201; PubMed-8905231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fam; PF00072; response_reg; 1. fam; PF00512; signal; 1.
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Pfam; PF02518; HATPase_c; 1.
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100.00%
1.30%
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01-JAN-1998 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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USH OR CG2762.
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9.00
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Best Local Similarity:
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DB:
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   REPARAMENT OF RE
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SEQUENCE FROM N.A.
MEDILINE-86278091; PubMed-2942540;
MEDILINE-86278091; PubMed-2942540;
Brown K.H., Brentano S.T., Donelson J.E.;
"Mung bean nuclease cleaves preferentially at the boundaries of
"Mung bean nuclease glycoprotein gene transpositions in trypanosome DNA.";
J. Blol. Chem. 261:10352-10358(1986).
EMBL; M14022; AAA30308.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5691;
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
(1971 2.4) variant surface glycoprotein TC gene (Fragment).
Trypanosoma brucei.
Genes Dev. 11:3083-3095(1997).

1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

R EMBL, 112322; CAA72991.1;

R EMBL, 122322; CAA72991.1;

R IJYBASS; FBER00003563; ush.

R PRINTS; PR00048; ZINCFINGER.

R PRINTS; PR00048; ZINCFINGER.

R PRINTS; SM00355; ZINC_FINGER_CZH2_2; 3.

R PRINTS; SM00355; ZINC_FINGER_CZH2_2; 3.

R PRINTS; PR00048; ZINC_FINGER_CZH2_2; 3.

R PRINTS; DR0048; ZINC_FINGER_CZH2_2; 3.

R PORN-binding; Nuclear protein; Zinc-finger.

R SEQUENCE 1191 AA; 124561 MW; C4C599C690C7096B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 AA; 1783 MW; 4A20FBE55CF59E5B CRC64;
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein ms11520.
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
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8.00
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Best Local Similarity:
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Best Local Similarity:
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01-NOV-1996 (TIEMBLIEL. 01, Created)
01-NOV-1996 (TIEMBLIEL. 01, Last sequence update)
01-DEC-2001 (TIEMBLIEL. 19, Last annotation update)
variable surface antigen (Fragment).
Trypanosoma brucei.
Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
                                                                                                                                                                                                                                                                                             "DNA rearrangements of the variable surface antigen genes of the Trypanosomes.";
                                                                                                                                                                                                         SEQUENCE FROM N.A.
BEDLINES 4242548; PubMed-6737319;
Murphy W.J., Brentano S.T., Rice-Ficht A.C., Dorfman D.M.,
Donelson J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                              68 AA; 7641 MW; 388437A80C8F5266 CRC64;
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                                                                                                                                                                                                                                                                                                                                                       J. Protozool. 31:65-73(1984).
EMBL; M31538; AAA30294.1; -.
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Servent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 1.16%
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Q9B134;
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                                                                                                                                                        Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Takaeuchi C., Tamada M., Tabata S., Sugimoto M., Complete genome structure of the nitrogen-fixing symblotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma
NCBI_TaxID~5691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Michels P.A.M., van der Ploeg L.H.T., Liu A.Y.C., Borst P.;
"The inactivation and reactivation of an expression-linked gene copy
for a variant surface glycoprotein in Trypanosoma brucei.";
EMBD. J. 3:1345-1351(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ol-MUV-1996 (TrEMBLrel. 01, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) Trypanosome brucel variable surface antigen 1.8 mRNA 3'-end (Fragment).
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EMBL; AP002997; BAB48874.1; -.

Hypothetical protein; Complete proteome.

SEQUENCE 48 AA; 5437 MW; 37A2002130817620 CRC64;
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Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
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                                                                                                        STRAIN-MAFF303099;
MEDLINE-21082930; PubMed-11214968;
               Phyllobacteriaceae; Mesorhizobium
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MEDLINE-84261425; PubMed-6086319;
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8.00
100.00%
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8.00
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Best Local Similarity:
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                                                                                      SEQUENCE FROM N.A
                                      NCBI_TaxID-381;
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01-NOV-1996
01-DEC-2001
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Q26036;
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ID 02
AC 02
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Length: Matches:

181 8.00

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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Cyprinella.
NCBI_TaxID=28791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=1, AND 2;
Grose M.J., Wiley E.O.;
"Phylogenetic relationships of the Hybopsis amblops species group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Teleostei: Cyprinidae).*;
submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
-! - CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
EMBL, AF216588; AAK34899.1; -.
EMBL, AF216590; AAK34891.1; -.
EMBL, FP00361; oxidored_q1.
Interpro. IPR001750; Oxidored_q1.
Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10071 MW; A0C6713C0C0B3879 CRC64;
880000
                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUAR-2002 (TrEMBLrel. 20, Last annotation update)
NADH dehydrogenase subunit 2 (Fragment).
Cyprinella lutrensis (red shiner).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
                                        Conservative:
Mismatches:
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Indels:
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100.00%
1.15%
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8.00
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Best Local Similarity:
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MEDLINE-96207227; PubMed-8619474;
Andersson B., Wentland M.A., Ricafrente J.Y., Liu W., Gibbs R.A.;
"A 'double adaptor' method for improved shotgun library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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Best Local Similarity:
                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                          Similarity:
                                                     construction.";
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Best Local Similar
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DB:
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STRAIN-CSTRL/63 TISSUB-TESTIS;

A REDLINE-21085660; PubMed=11217851;
A Rawal J., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
A Arakawa T., Shinaqawa A., Shibata K., Yoshino H., Adachi J., Fukuda S.,
A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Rasukawa T., Saito R.,
A Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Rieschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
A Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Brownstein M.J., Bult C., Fletcher C., Fullia M., Gariboldi M.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fullia M., Gariboldi M.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodiiguez I., Sakamoto N.,
Sazaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Nyasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wanshaw-Bonis A., Yoshida K., Hasegawa Y., Kawaji H., Rohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10763 MW; 7C7BC18D7E859890 CRC64;
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Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Matches:
Conservative:
Mismatches:
Indels:
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CTGGGCCTGCTGCCAGTTGCCCCA 1424
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             79 LeuGlyLeuLeuProValAlaPro 86
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100.00%
1.15%
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                                                                                    PRELIMINARY;
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                                                                                                                                                        4930442H23R1k protein.
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hayashizaki Y.;
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                                                                                      09D5G7
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043202
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Q9D5G7
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MEDLINE-93188700; PubMed-8446027;
Eiglmeier K., Honore N., Woods S.A., Caudron B., Cole S.T.;
"Use of an ordered cosmid library to deduce the genomic organization
of Mycobacterium leprae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium leprae.
Bacteria: Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
                                                                                        Yu W., Andersson B., Worley K.C., Muzny D.M., Ding Y., Liu W., Ricafrente J.Y., Wentland M.A., Lennon G., Gibbs R.A.; "Large-scale concatenation cDNA sequencing."; Genome Res. 7:353-358(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Oliver K., Harris D.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 protein.
111 AA; 12241 MW; 13DD36663FDF0B8C CRC64;
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                                                                                                                                                                                                                                                                                                   104
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01-JUL-1997 (TYEMBLIAEL: 04, Last sequence update)
01-NOV-1998 (TYEMBLIAEL: 08, Last annotation update)
Hypothetical 12.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                     InterPro; IPR003140; PLP_Cesterase.
Pfam; PF02230; abhydrolase_2; 1.
NON TER 1 1
                                                              FISSUE-BRAIN;
MEDLINE-97264341; PubMed-9110174;
Anal. Biochem. 236:107-113(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mol. Microbiol. 7:197-206(1993).
EMBL; 296801; CAB09641.1;
                                                                                                                                                                                                                                                SEQUENCE 104 AA; 11403 MW;
                                                                                                                                                                       EMBL; AF035293; AAB88180.1; -
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8.00
100.00%
100.00%
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8.00
100.00%
100.00%
1.16%
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Plasmid 44:285-291(2000).
                            SEQUENCE FROM N.A.
                                            STRAIN-22243;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                     STRAIN-ATCC 15692 / PAO1;
MEDLINE-20437337; PubMed=10984043;
Stover C.K., Pham X. O.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Stover C.K., Pham X. O.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.M., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tauch A., Puhler A., Kalinowski J., Thierbach G.;
"TetZ, a New Tetracycline Resistance Determinant Discovered in Gram-
Positive Bacteria, Shows High Homology to Gram-Negative Regulated
Efflux Systems.";
                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=1718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          opportunistic pathogen.";
Nature 406.959-964(2000).
EMBL; AROU4503; ARG04060;
Hypothetical protein; Complete proteome.
SEQUENCE 143 AA; 15028 MW; 0235C65ECEDCF3DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Corynebacterium glutamicum (Brevibacterium flavum). Plasmid R-plasmid pAG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                Last sequence update)
Last annotation update)
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Mismatches:
Indels:
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Matches:
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                                          1392 CTGGCTCGGGCAGCAGGTTCCGCC 1369
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              US-09-824-647-16 (1-2095) x 007154 (1-111)
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                                                          Created)
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                                                                                                                                                                (TrEMBLrel. 16, C
(TrEMBLrel. 16, L
(TrEMBLrel. 18, L
                                                                                                                                                                                           01-OCT-2001 (TrEMBLrel. 18, Hypothetical protein PA0679.
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8.00
100.00%
100.00%
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16
                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                             Seudomonas aeruginosa.
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Best Local Similarity:
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Pred. No.:
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01-MAR-2001
                                                                                                                                                                                                                                                                            Pseudomonas
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Q915P6;
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Coat protein; Envelope protein; Glycoprotein; Nonstructural protein; Polyprotein; Transmembrane.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Genome polyprotein [Contains: envelope glycoprotein E2 (GP68) (GP70)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
--- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E1.
EMBL. AR422337; AAL24649.1; -.
InterPro; IPR002599; HCV. env.
InterPro; IPR002531; HCV_NS1.
                                                   31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=ACL-92;
Lyra A.C., Fan X., Di Bisceglie A.M.;
"Evolution of hepatitis C viral quasispecies after liver
Tauch A.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF121000; AAD25068.1;
InterPro; IPR003795; DUF192.
Pfam; PF02643; DUF192; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C4F5DA7B61F6C484 CRC64;
                                                                                                    149 AA; 15897 MW; 398307CEEC67DA4D CRC64;
                                                                                                                                                            149
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Matches:
Conservative:
Mismatches:
Indels:
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Mismatches:
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154 AA; 16728 MW;
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Pfam; PF01560; HCV_NS1; 1.
ProDom; PD186062; HCV_NS1; 1.
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Best Local Similarity:
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Hepatitis C virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transplantation.
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Best Local Similari
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Matches:
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EMBL, AE001303, AAC67886.1; --
Hypothetical protein; Complete
SEQUENCE 171 AA, 19423 MW;
                                                                                                                                                                                                                                                                                              084305;
01-NOV-1998 (TrEMBLrel. 08, Cr
01-NOV-1998 (TrEMBLrel. 08, La
01-MAR-2002 (TrEMBLrel. 20, La
Hypothetical protein CT303.
CT303.
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            Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
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084305
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      Score:
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Genome polyprotein [Contains: envelope glycoprotein E2 (GP68) (GP70)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probom; PD186062; HCV_NS1; 1.
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; Transmembrane.
NON_TER 1
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Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                            Hepatitis C'virus.
Viruses: ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                            Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: TO HERPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E1.
EMBL; AF422338; AAL24650.1; -
InterPro; IPR002519; HCV_env.
InterPro; IPR002531; HCV_env.
Pfam; PP01539; HCV_env; 1.
pfam; PP01530; HCV_env; 1.
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                                                                                                                                                                                                                                                                                                                    .yra A.C., Fan X., Di Bisceglie A.M.;
Evolution of hepatitis C viral quasispecies after liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases EMBL; AF497310; AAM19566.1;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Matches:
Conservative:
Mismatches:
Indels:
                                             154 AA.
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154 AA; 16756 MW;
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                transplantation.
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Pred. No.:
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SEQUENCE
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SEQUENCE
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-20150255, PubMed-10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weldman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Eisen J., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-D/UW-3/CX;
MEDLINE-99000809; PubMed-9784136;
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
Mitchell W.P., Olinger L., Tatusov R.L., Shao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome sequence of an obligate intracellular pathogen of humans:
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3CB88DD2D08B24BF CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical protein TC0577.
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Last annotation update)
80000
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_FaxID-83560;
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia
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Matches:
Conservative:
Mismatches:
                 Conservative:
Mismatches:
Indels:
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Entil J. Artifreezell.

PRINTS; PRO0308; ANTIFREEZEI.
Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                      pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
EMBL, AE0023256; AAF39412.1; -.
TICR, TCO577; -.
Hypothetical protein; Complete proteome.
SEQUENCE 178 AA; 20384 MW; 5D11D1EA77B3DE39 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Probable transmembrane protein.
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
                                                                                                                                                                                                                                                                                                      Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
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Best Local Similarity:
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SEQUENCE 188 AA;
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Best Local Similarity:
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                                                                                                                                                                                                                   Alignment Scores:
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STRAIN-A3(2) / M145;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,
Warren T., Mietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                         Ti.
                                                                                                                                                               Davison A.J., Akter P., Dolan A., Wright K.M., Addison C., Alcendor D.J., Hayward G.S., McGeoch D.J.;
"The human cytomegalovirus genome revisited.";
submitted (FEB-2002).
EMBL, AF480881, AMM00677.1;
SEQUENCE 190 AA, 21528 MW, E918F4FC02CEDD78 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C7ACFE12E7BE4B4C CRC64;
                                       chimpanzee cytomegalovirus.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Veraherpesvirinae; Cytomegalovirus.
NCBL_TaxID=188763;
  (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-001-2000 (TrEMBLrel. 15, Created)
01-001-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein SC02957.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-824-647-16 (1-2095) x Q8QS62 (1-190)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL138851; CAB72203.1;
                                                                                                                                                                                                                                                                                                                                        163
8.00
100.00%
100.00%
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1.16%
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                 regument protein UL26
                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
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01-JUN-2002
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Q9L1T8;
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SEQUENCE FROM N.A.
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                                                                                     EMBL;
                                                                                                   EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.B., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., HcDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1998 (TIEMBLE). 08, Last sequence update)
01-MAR-2002 (TIEMBLE). 20, Last annotation update)
Lysophospholipase (Acyl-protein thioesterase-1) (Lysophospholipase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Не К.,
                                                                                   "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Devedjiev Y., Dauter Z., Kuznetsov S.R., Jones T.L., Derew
"Crystal Structure of the Human Acyl Protein Thioesterase
Single X-Ray Data Set to 1.5 A.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hu G.;
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Human lysophospholipase gene.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                             23653C80086FCB32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Shen Y., Guan Z., Gu J., Ye M., Zhou J., Zhang Q., Xu
Chen S., Mao M., Chen Z.;
                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                              1370 GCGGAACCTGCTGCCCGAGCCAGG 1393
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01-NOV-1998 (TrEMBLrel. 08, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last ann
                                                                                                                                                          InterPro; IPR000345; CytC_heme_bind.
InterPro; IPR003088; Cyt_CI.
InterPro; IPR002329; Cyt_CIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                Pfam; PF00034; cytochrome_c; 2.
RNTWTS; PR00060; CYTCHROMECIC.
PRODOM; PD004020; CYT_CTC; 2.
PROSITE; PS00190; CYTOCHROME_C; 2.
                                                                                                                                                                                                                                            Complete proteome.
                                                                                                            Science 286:1571-1577(1999).
EMBL; AE002078; AAF12028.1; -
HSSP; Q52369; 1ETP.
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8.00
100.00%
100.00%
1:15%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
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TISSUE-BONE MARROW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
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                                                                           Fraser C.M.;
                                                                                                                                                                                                                                                                                       Alignment Scores:
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Calculum-independent phospholipase A2 isoform 2.
Oryctolagus cuniculus (Rabbit).
Cukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Portilla D., Crew M.D., Grant D., Serrero G., Bates L.M., Dai G., Sasner M., Cheng J., Buonamo A., "CDNA cloning and expression of a novel family of enzymes with calcium-independent phospholipase A2 and lysophospholipase
                                                                              3:
Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF081281; AAC31610.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PSO0339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
SROUENCE 230 AA; 24687 MW; 89AF2017AEFC9FAC CRC64;
                                                                                                                                                                                                                                      90C0522F765F1AC6 CRC64;
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Conservative:
Mismatches:
Indels:
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Mismatches:
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Matches:
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EMBL; U97148; AAC63432.1; -.
HSSP; Q53547; IAUO.
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InterPro; IPR003140; PLP_Cesterase.
InterPro; IPR000379; Ser_estrs_site.
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                                                                                                                                                                            nterPro; IPR003140; PLP_Cesterase.
InterPro; IPR00379; Ser_estrs_site.
FF02230; abhydrolase_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1998 (TrEMBLrel. 08, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-98308497; PubMed-9644627;
                                                                              AAG10063.1; -.
AAH10397.1; -.
AAH08652.1; -.
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                                                           AAD26993.1;
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8.00
                                                                                                                                                              MA-2DPAGE; 075608; -.
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Best Local Similarity:
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                                                               AF077198;
                                                                                                                       BC008652;
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                                                                                AF291053
                                                                                                      BC010397
                                                                                                                                         053547;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                activities."
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RESULT 33

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RX MEDLINE-21085660; PubMed=11217851;
RA Arakwa T., Shidata K., Yoshino M., Itoh M., Ishii Y., Rawai J., Shidagawa A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Rakawa T., Hara A., Fukunishi Y., Konno H., Adawa K., Tawa M., Nishil K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Rasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., RA, Fuehl P., Lewis S., Matsuo Y., Mikaido I., Pesole G., Quackenbush J., Ra Kuehl P., Lewis S., Matsuo Y., Mikaido I., Pesole G., Quackenbush J., Ra Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Ra Sakai K., Okido T., Furuno M., Aono H., Bäldarelli R., Barsh G., Rashai K., Okido T., Furuno M., Aono H., Bäldarelli R., Barsh G., Bornstein M.J., Buit C., Fletcher C., Fujita M., Gariboldi M., Rusharotcher S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., A. Nordone P., Ring B., Ringwald M., Rodriquez I., Sakamoto N., Asaaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., A. Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., A. Havashizaki V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
-1- CATALYTIC ACTIVITY: 2-LYSOPHOSPHATIDYLCHOLINE + H(2)
GLYCEROPHOSPHOCHOLINE + A FATTY ACID ANION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230 AA; 24687 MW; 89AF2017AEFC9FAC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TYEMBLrel. 13, Created)
01-MAY-2000 (TYEMBLrel. 13, Last sequence update)
01-MAY-2000 (TYEMBLrel. 13, Last annotation update)
CG5767 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF02230; abhydrolase_2; 1.
PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1686 CTGTCCTGCTGCCTTCCGCTGCGC 1709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002106; AATRNA_ligaseII.
InterPro; IPR003140; PLP_Cesterase:
InterPro; IPR00319, Ser_estrs_site.
Pefm. PR02230; abhydrolase 2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-824-647-16 (1-2095) x P97823 (1-230)
                                                                                                                     STRAIN-C57BL/6J; TISSUE-KIDNEY;
MEDLINE-21085660; PubMed-11217851;
                                       Deems R.A., Dennis E.A.;
Chem. 0:0-0(0).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U89352; AAB48627.1; -. AK002674; BAB22276.1; -. BC013536; AAH13536.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.00%
100.00%
1.15%
11
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MGD; MGI:1344588; Lyplal.
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Best Local Similarity:
[1]
SEQUENCE FROM N.A.
                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=KIDNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rydrolase.
                                           Wang A.,
J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score:
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01-MAR-2002 (TrEMBLE). 20, Last annotation update)
LPHOSPHOLIPASE 1A (EC 3.1.1.5) (Lysophospholipase I) (LECITHINASE B)
(LYSOLECTIFILNASE) (Phospholipase B) (Adult MALE kidney CDNA, RIKEN
FULL-length enriched LIBRARY, clone:0610025N20, FULL INSERT sequence)
                                                                                                                                                                                                                                                                                                                                                                                                                    "Purification, cDNA cloning, and regulation of lysophospholipase from rat liver.";
                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-98308497; PubMed-9644627; Portilla D., Crew M.D., Grant D., Serrero G., Bates L.M., Dai G., Sasner M., Cheng J., Buonanno A., "Cheng J., Buonanno A., "chang and expression of a novel family of enzymes with calcium-independent phospholipase A2 and lysophospholipase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
230 AA; 24709 MW; AAFEBC4702EAAD74 CRC64;
                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                          230 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Am. Soc. Nephrol. 9:1178-1186(1998).
EMBL; D63885; BAA09935.1; -.
EMBL; U91146; AAC63430.1; -.
HSSP; Q53547; 1AUO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
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                                                                                                                                                                                                                                                                                                                                                          STRAIN-WISTAR; TISSUE-LIVER;
MEDLINE-96205961; PubMed-8631810;
Sugimoto H., Hayashi H., Yamashita S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interpro; IPR002106; AAtRNA_11gaseII.
InterPro; IPR003140; PLP_Cesterase.
InterPro; IPR00379; Ser_estrs_site.
Pfan; PF02230; abhydrolase_2; I.
PROSITE; PS00339; AA_TRNA_LIGASE_II_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-824-647-16 (1-2095) x P70470 (1-230)
  Created)
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                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biol. Chem. 271:7705-7711(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1997 (TrEMBLrel. 03,
                                                                                                                                               01-FEB-1997 (TrEMBLrel. 02, 01-FEB-1997 (TrEMBLrel. 02, 01-MAR-2002 (TrEMBLrel. 20, LYSOPHOSIPASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.00%
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8.00
                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                               NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LYPLA1 OR PLA1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
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SEQUENCE

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Query Match: DB:

P97823

RESULT 34

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Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
            Deinococcaceae; Deinococcus.
NCBI_TaxID-1299;
                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29ATL6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adams M.D., Celniker S.E., Holt R.A. Frans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A. Frans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A. Frans C.A., Gocayne J.D.,
RA Gorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Ratton G.G., Wortman J.R., Yandell N.D., Zhang Q., Chen L.X.,
Ratton R.C., Rogers Y.-H.C., Blazej R.G., Change M., Edelfer B.D.,
RA Sutton G.G., Wortman J.R., Zandell N.D., Zhang Q., Chen L.X.,
RA Sutton R.C., Rogers Y.-H.C., Blazej R.G., Change M., Petelifer B.D.,
Randon R.C., Rogers Y.-H.C., Blazej R.G., Change M., Baldwin D.,
Rallow R.M., Basu A., Baxendale J., Baytaktaroll L., Bealstey E.M.,
Randow R.Y., Benco P.V., Berman B.P., Bhandari D., Bolshakov S.,
Burtis R.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,
Randerry J.M., Cawley S., Dallike C., Davenport L.B., Davies P.,
Randerry J.M., Cawley S., Dallike C., Davenport L.B., Davies P.,
Randon R.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischman R.,
Rodek A., Goof F. Gorrell J.H.G., Gua P., Hernandez J.R., Houck J.,
Randle B.E., Medirer A., Howland T.J., Hernandez J.R., Houck J.,
Randle B.E., Kodira C.D., Kraft C., Kravitz S., Mush D., Lai Z.,
Lux, Mattel B., McIntosh T.C., McLeod M.P., McPherson D.L.,
Randle B.E., Kodira C.D., Kraft C., Kravitz S., Wolph D., Lai Z.,
Lux, Mattel B., McIntosh T.C., McLeod M.P., McPherson D.K.,
Runt S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.K.,
Runt S.M., Moy M., Murphy B., Murphy L., Warany D.M., Nelson D.K.,
Rhourt S.M., Moy M., Murphy B., Murphy L., Warany D.M., Nelson D.K.,
Rhourt S.M., Moy M., Murphy B., Murphy L., Warany D.M., Nelson D.K.,
Rhourt S.M., Woodage T., Stapleton M., Stupski M.P., Shu B.,
Rhort S.M., Woodage T., Stapleton M., Stupski M.P., Shu B.,
Rhourt S.M., Woodage T., Stapleton M., Stupski M.P., Shu B.,
Rhourt S.M., Woodage T., Stapleton M., Stupski M., Rhyers S., Nelp D.,
Rhyers R., Realington K., Stapleton M., Stupski M., Rhyers R., Rhyers E.W., Rodong T., Worley K., Wu B., Shu B.,
Rhyers E.W., Salener S., S
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25956 MW; 22A35668145C1946 CRC64;
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Last annotation update)
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transcriptional regulator, ICLR family.
                Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1208 ACCACCAGCACTGCTGCCCCCAGC 1231
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                                                                           STRAIN-BERKELEY;
MEDLINE-20196006; Pubmed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2002 (TrEMBLrel. 20,
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100.00%
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1.15%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Delnococcus radiodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FBgn0034292:
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Query Match:
                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FlyBase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 36
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIINE-21140306; PubMed-11244102;
Chaumont F., Barrieu F., Wojcik E., Chrispeels M.J., Jung R.;
"Aquaporins constitute a large and highly divergent protein family in
malze.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE MIP/AQUAPORIN FAMILY (TC 1.A.8).
EMBL; AF336505; AAK26772.1; -.
HSSP; P29972; IFQY.
                                   White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Petersog J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Woffat K.S., Qin H., Jiang L., Panphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.I. Ferthum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                            Science 286:1571-1577(1999).
                                                                                                                                                                                                                        "Genome sequence of the radioresistant bacterium Delnococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA-binding; Transcription regulation; Complete proteome.
SEQUENCE 253 Aa; 27299 MW; DBB8F05ABE6F65A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26519 MW; DDD4C1AC3E7DB8D1 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Tonoplast membrane integral protein ZmTIF4-1.
Zea mays (Maize)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches:
Conservative:
Mismatches:
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                  MEDLINE-20036896; PubMed-10567266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plant Physiol. 125:1206-1215(2001)
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ProDom; PD000295; MIP_family; 1.
PROSITE; PS00221; MIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR000425; MIP_family. Pfam; PF00230; MIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000285; HTH_ICLR.
Pfam; PF01614; ICLR; 1.
SWART; SM00346; HTH_ICLR; 1.
                                                                                                                                                                                                                                                                                                                                                     EMBL; AE001862; AAF12212.1; -. TIGR; DRA0152; -.
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8.00
100.00%
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                         radiodurans R1.
                                                                                                                                                                                                   Fraser C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
STRAIN-R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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STRAIN-A3(2) / M145;
STRAIN-A3(2) / M145;
Bertley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Bertley S.D., Chater K.P., Harris D.E., Quail M.A., Kieser H.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Rarper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Bornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Nell S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coelicolor A3(2).";
Nature 417:141-147(2002).
-1- SIMILARITY: BELONGS TO THE ARAC/XYLS FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
Kinashi H., Hopwood D.A.;
A set of ordered cosmids and a detailed genetic and physical map ithe 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
PROSITE; PS01124; HTH_ARAC_FAMILY_2; 1.
NRA-binding; Hypothetical protein; Transcription regulation.
SEQUENCE 256 As; 27761 MW; 1971B47CBEB684C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S.D., Barrell B.G., Rajandream M.A.;
to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oliver K., Harris D.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                        01-006-1998 (TrEMBLrel. 07, Last sequence update) 01-00N-2002 (TrEMBLrel. 21, Last annotation update) Hypothetical protein SC06425.
    Conservative:
                        Mismatches:
Indels:
                                                              Gaps:
                                                                                                                                      1544 CTACGGGCCAGGAAGGTGGCAGGC 1521
                                                                                                  US-09-824-647-16 (1-2095) x Q9PA28 (1-256)
                                                                                                                                                            01-AUG-1998 (TrEMBLrel. 07, Created)
                                                                                                                                                                                                                                                        PRT;
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MEDLINE-97000351; Pubmed-8843436;
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InterPro; IPR000005; HTHARAC.
Pfam; PF00165; HTH_ARAC.
  100.00%
100.00%
1.16%
16
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SMART; SM00342; HTH_ARAC;
                                                                                                                                                                                                                                                    PRELIMINARY;
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8.00
                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces coelicolor.
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Parkhill J., Bentley
Submitted (JAN-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1902;
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Pred. No.:
Score:
                                                                                                                                                                                                                                                        069819
                                                                                                                                                                                                                    RESULT 39
                                                                                                                                                                                                                                        069819
                                                                                                                                                                                                                                                                          Alvarenga R., Alves L.M.C., Araya J.E., Band G.S., Baptista C.S., Rarros, M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S., Bueno W.R.P., Camargo A.A., Camargo L.E., Bardin G.S., Baptista C.S., Bueno W.R.P., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M., Coltino C., Costa F.F., Costa M.C.R., Costa-Neto C.M., Rochardon L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H., Franca S.C., Franco M.C., Frohme M., Furlan L.R., Racincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A., Rarnoco M.C., Frohme M., Furlan L.R., A darnier M., Goldman M.H.S., Gomes S.L., Gruber A., H. P. P.L., Hoheisel J.D., Junqueira M.D., Kemper E.L., Kitajima J.P., R. Krieger J.E., Kuranae B.E., Laigret F., Lambais M.R., Leite L.C.C., R. Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Matsukuma J.P., Marchins E.A.L., Martins E.M.F., Matsukuma J.Y., Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y., Mondon D.H., Nagail M.A., Nascimento A.L.T.O., Netto L.E.S., Mania A. Jr., Nobrega F.G., Mines L.R., Oliveira M.A., de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A., A de Suza M.J.M., de Souza A.J.M., a Sluye M.A., Terenzi M.F., Truffi D., Tsai S.N., Tsuhako M.H., R. Zago M.A., Zatz M., Meidanis J., Setubal J.C., Satubal J.C., Statubal J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4F21E7001BA1265B CRC64;
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                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                            Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                256 AA.
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Matches:
                            Length:
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                                                                                                                        Gaps:
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InterPro; IPR003249; U_glycosyl.
Pfam; PF03167; UDG; 1.
                                                                                                                                                            US-09-824-647-16 (1-2095) x Q9ATL6 (1-255)
                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-20365717; PubMed-10910347;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD001589; U_glycosyl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE004075; AAF85489.1; -.
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Alvarenga R., Alves L.M.C., Ar
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                        158
8.00
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1.16%
                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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8.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xylella fastidiosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome. SEQUENCE 256 AA;
                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-2371;
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      Alignment Scores:
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Pred. No.:
Score:
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                                                                                                Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                    Q9PA28;
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                        Pred. No.:
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US-09-824-647-16 (1-2095) x Q39263 (1-259)
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     Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Ward M.J., Lew H., Treuner-Lange A., Zusman D.R.;
"Regulation of motility behavior in Myxococcus xanthus may require an extracytoplasmic-function sigma factor.";
EXECT: 180:5668-567[1998].
EXEL: AF049107; AAC98489.1;
                                                                                                                                                                                                                                                                                                            MEDILINE-96347136; PubMed-8736543;
Trudeau R.G., Ward M.J., Zusman D.R.;
"Identification and characterization of FrzZ, a novel response regulator necessary for swarming and fruiting-body formation in Myroconcus xanthus.";
                                                                                                                                                                                                                                          Bacteria; Proteobacteria; delta subdivision; Myxobacteria; Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus.
NCBL_TaxID=34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ll protein.
257 AA; 28575 MW; 860E35015266C7EB CRC64;
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Last annotation update)
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 28.6 kDa protein.
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 Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
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                                      Gaps:
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                                                                                 US-09-824-647-16 (1-2095) x 068521 (1-257)
                                                          US-09-824-647-16 (1-2095) x 069819 (1-256)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequ
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                                                                                                                                                                                                                                                                                                                                                                 Myxococcus xanthus.";
Mol. Microbiol. 20:645-655(1996).
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                                                                                                                                                                                                                               Myxococcus xanthus.
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Best Local Similarity:
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                                                                                                                                  RESULT 40
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MEDLINE-21140306; PubMed-11244102;
Chaumont F., Barrieu F., Wojcik E., Chrispeels M.J., Jung R.;
"Aquaporins constitute a large and highly divergent protein family in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pague B.W., Goodman H.M.;
characterization of a family of Arabidopsis zinc finger protein
                                                                                                  (BY
(TC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA-Dinding; Metal-binding; Zinc-finger.
SEQUENCE 259 AA; 28644 MW; AE8F1B4A280067FD CRC64;
                                                                                                                                                                                                                                                                                                       465414DFCB7F7BE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                               257
8
0
0
0
                                                                         Plant Physiol. 125:1206-1215(2001).
-!- SUBCELLUIAR LOCATION: INTEGRAL MEMBRANE PROTEIN
-!- SIMILARITY: BELONGS TO THE MIP/AQUAPORIN FAMILY
EMBL; AF326506; AAR26773.1; -.
InterPro; IPR000425; MIP_family.
Pfon; PF00230; MIP: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TIEMBLrel. 01, Created)
(TIEMBLrel. 01, Last sequence update)
(TIEMBLrel. 20, Last annotation update)
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00096; zf-C2H2; 1.
MARRY: SM00355; znF_C2H2; 1.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1362 GCAGCTGGTGTGCTGGTCACAGCC 1339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-LANDSBERG ERECTA; TISSUE-ROOT; MEDLINE-95322589; PubMed-7599312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-824-647-16 (1-2095) x Q9ATL5 (1-257)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant Mol. Biol. 28:267-279(1995).
EMBL, 139647; ARA87300.1; -.
TRANSFAC; TO9565; -.
INTERPIC: IPRO00822; Znf_C2H2.
                                                                                                                                                                                                                   PRINTS, PRO0783; MINTRINSICP.
PRODOM; PD000295; MIP_family;
PROSITE; PS00221; MIP, 1.
Transmembrane; Transport.
SEQUENCE 257 AA; 26603 MW;
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
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01-NOV-1996 (
01-MAR-2002 (
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1219 AGTGCTGGTGCTCGAGCAGCAG 1196
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TO STRAIN—CV. STRAIN—CO., ELONARY A., CHOR C. M., BECOKS S.Y.,

TO STRAIN—CV., COND L., CONDAY A.R., CERASY T.H., DEWAR K.,

TO DIND P., Etgu P., Feldblyum T.V., Feng J.-D., Fulli C.Y.,

TO DIND P., Etgu P., Feldblyum T.V., Feng J.-D., Hughes B., Hulzar L.,

TO STRAIN—CV., TO STRAIN—CV., TO STRAIN—CV., MAD S., KABAKIN E.,

TO STRAIN—CV., TO STRAIN—CV., LI J.H., LI Y.-P.,

TO STRAIN—CV., MIRADA M., NGUNEN M., NGATZIAI A.,

TO STRAIN—CV., TO STRAIN—CV., STRAIN—CV., OSDOTHO B.I.,

TO STRAIN—CV., TO STRAIN—CV., STRAIN—CV., OSDOTHO B.I.,

TO STRAIN—CV., TO STRAIN—CV., STRAIN—CV., OSDOTHO B.I.,

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Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicacee; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shinn P., Chen H., Cheuk R., Kim C.J., Banh J., Bowser L., Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Mir Kada M., Narusaka M., Nguyen M., Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M., Seki M., Southwick A., Toriumi M., Yamada K., Yu G., Shinozaki K., Davis R.W. Theologis A., Ecker J.R., "Arabidopsis cDMA clones."; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Koesema E., Chen H., Cheuk R., Kim C.J., Meyers M.C., Shinn P., Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A., Kazlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M., Ondera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C.; Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S.,
                                                                                                                                                                                                        ol-WAR-2002 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
C2H2-type zinc finger protein, putative (Atlg66140/F15E12_19).
F15E12.19.
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Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                              260 AA
1269 TCCTCGCTGACACTGCCCCTCAGC 1246
                         (TrEMBLrel. 17, Created)
                                                                                                                                         PRT;
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                                                                                                                                            PRELIMINARY;
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                                                                                            RESULT 43
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STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
05JNBA0026J14.33 protein (OSJNBA0042P21.8 protein).
05JNBA0026J14.33 OR OSJNBA0042P21.8.
07rza sativa (laponica cultivar-group).
Eukaryota, viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                          34.
                              EMBL; AC026480; AAG51296.1; --
EMBL; AC026480; AAG51296.1; --
EMBL; AC026480; AAG51296.1; --
EMBL; AC026480; AAG51296.1; --
EMBL; AV058087; AAL24195.1; --
EMBL; AV058087; AAL06967.1; --
InterPro; IPR000822; Znf_CZH2.
InterPro; IPR000822; Znf_CZH2.
Pfam; PF00096; Znf_CZH2, 1.
PROSITE; PS0026; ZINC_FINGER_CZH2_1; 1.
PROSITE; PS0167; ZINC_FINGER_CZH2_2; 1.
PROSITE; PS0167; ZINC_FINGER_CZH2_2; 1.
SMART; ZNG_FINGER_CZH2_2; 1.
SROUFNCE 260 AA; 28308 MW; 48484EC120250F09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone:OSJNBa0026714.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
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Theologis A., Ecker J.R.;
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Mismatches:
Indels:
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Matches:
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Shinozaki K., Davis R.W., '
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115 SerAlaGlyGlyProSerSerArg 122

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01-UUN-2001 (TrEMBLrel. 17, Created)
01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
Transcription factor MRG1.
Transcription factor MRG1.
Eattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                      huang D.Z., Chou Y.-T., Yang Y.-C.; Structural and functional conservation of MRG family in system
                                                                                                                                                                                                                                                                                                                                              evolution.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF361476; AAK30621.1; -
SEQUENCE 269 AA; 28291 MW; 038DC4B21E4E21F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                        269 AA.
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                                        PRT;
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8.00
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STRAIN-SPRAGUE-DAWLEY;
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Best Local Similarity:
Query Match:
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RESULT 45
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Sequence

Sequence 113, Sequence 113, Sequence 113,

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Sequence 113, App Sequence 6, Appli

Seguence 80,

Patent No.

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Title: Perfect score:

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Run 8

Scoring table:

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Sequence Sequence Sequence

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APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996-488/POSON PROPERTION NUMBER: US/O8/991,862
CURRENT APPLICATION NUMBER: US/O8/991,862
CURRENT FILING DATE: 1998-08-17
EARLIER APPLICATION NUMBER: 08/863,862
EARLIER PILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: PEPTIDE
LOCATION: (1)..(14).
OCHER INFORMATION: Internal peptide of human GP88 used to develop
OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1708 GCACGCAGGGTACCAAGTGTTTGCGCAGGGAGGCCCCGCGC 1749
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Matches:
Conservative:
Mismatches:
Indels:
                                         US-08-933-843-113
US-08-934-223-113
US-09-348-952A-5
US-09-413-492-113
US-09-053-611-6
                                                                                                               5470825-3
US-08-847-844A-80
US-09-220-528-91
US-09-6461-697-66
US-09-461-697-66
US-08-672-850-19
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US-08-602-999A-82
US-08-278-865 382
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US-09-120-365-82
                              US-08-934-224-113
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JS-09-248-061B-9
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US-09-120-365-84
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-O-/cgn2_1/USPTO_spool/US09824647/runat_07072003_154800_26631/app_query.fasta_1.2247
-O-/cgn2_1/USPTO_spool/US09824647/runat_07072003_154800_26631/app_query.fasta_1.2247
-O-/cgn2_1/USPTO_spool/US09824647/runat_07072003_154800_26631/app_query.fasta_1.2247
-DB-1581004_Patents_AA -OFMTP-fasta -SUFFIX-1im.rai -MINMATCH-0.1 -LOOPCIL-0
-LOOPEXT-O -UNITS-bits -START-1 -MATRIX-oligo -TRANS-human40.cdi
-LIST-45 -DOCALIGN-200 -THR.SCORE-quality -THR.MINF-1 -ALIGN-45 -MODE-LOCAL
-OGTERT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-15
-NOLMARA -LARGEQUERY -NEG_SCORES-0 -WAIT -DSPBLOCK-100 -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPDF-60 -XGAPEXT-60 -FGAPOP-6
-FGAPEXT-7 -YGAPOP-60 -YGAPEXT-60 -DELOP-6 -DELEXT-7
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Sequence 39, Appli
Sequence 7, Appli
Sequence 5, Appli
Sequence 113, App
Sequence 113, App
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5470825
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Sequence 2, Appli
                                                                                                               (without alignments)
4251.105 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                      cgcaggcagaccatgtggac.....ataaagtttgtcactttctt 2095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2,
Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3
                                                                                               July 7, 2003, 16:00:43; Search time 29 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
3: /cgn2_6/ptodata/1/laa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                   using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-991-862-7
US-08-245-853-2
US-08-573-675-2
5470825-2
US-08-991-862-5
US-09-419-826-39
US-08-244-951A-7
US-08-244-951A-7
US-08-234-22-113
US-08-933-402-113
US-09-207-621-113
US-09-207-621-113
                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                      262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                               60.0 , Xgapext 60.0
60.0 , Ygapext 60.0
6.0 , Fgapext 7.0
6.0 , Delext 7.0
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                                                                                                                                                    US-09-824-647-16
694

    protein search,

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Match Length
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Xgapop
Ygapop
Fgapop
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Score

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Result

Database

Sequence 4, Sequence 17,

Sequence

Sequence

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APPLICANT: SCOTT, RANDY W.; GLEICH, GERALD J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WILDE, CRAIG G.
TITLE OF INVENTION: BASOPHIL GRANULE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-824-647-16 (1-2095) x US-08-573-675-2 (1-15)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-824-647-16 (1-2095) x 5470825-2 (1-15)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/259,564
FILING DATE: 15-JUN-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 551,263
FILING DATE: 10-JUL-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 8
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
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LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-573-675-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5470825-2
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11
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: SCOTT, RANDY W.
APPLICANT: GLEICH, GERALD J.
APPLICANT: WILDE, CRAIG G.
APPLICANT: WILLE, CRAIG G.
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              865 GACATGGAGGTGAGCTGCCCAGATGGCTATACC 897
                                                                                                                                         APPLICANT: SCOTT, RANDY W.
APPLICANT: GLEICH, GERALD J.
APPLICANT: WILDE, CRAIG G.
TITLE OF INVENTION: BASOPHIL GRANULE PROTEINS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-824-647-16 (1-2095) x US-08-245-853-2 (1-15)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 24842-20059.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEPA: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      datches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,813
FILING DATE: 11-SEP-1992
ATORNEY/GENT INFORMATION:
NAME: BOZICEVIC, KARL
REGISTRATION NUMBER: 28,807
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/245,853
                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08573675
Patent No. 5747283
GENERAL INFORMATION:
                                                                                                                                                                                                                                                      F: MORRISON & FOERSTER 755 Page Mill Road
                                                                                          Sequence 2, Application US/08245853
Patent No. 5476839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                           CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                 X: USA
94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-573-675-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
                                                                RESULT 2
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Conservative: Mismatches: Indels:

11.00 100.00% 100.00% 1.59%

Gaps:

Length:

5470825

Pred.

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Matches: Conservative: Mismatches:

0.159 11.00 100.00% 100.00%

Length:

Indels:

Gaps:

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SSEE: Fish & Richardson
F: 2200 Sand Hill Road, Suite 100
Menlo Park
: California
                                                                                                                                                                                                            SOUTWARE:
SOUTWARE:
APPLICATION DATA:
APPLICATION NUMBER: US/08/573,675
FILING DATE: 18-DEC-1995
CLASSIFICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION NUMBER: US 07/943,813
APPLICATION NUMBER: US 07/943,813
APPLICATION NUMBER: US 07/943,813
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 05514/01300
TELEPHONE: (415) 322-5070
TELEPHONE: (415) 322-5070
TELEPHONE: (415) 824-0875
INFORMATION FOR SECULD NO: 2:
                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                          COUNTRY:
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us-09-824-647-16.lim.rai

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COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/08244951A Patent No. 5843779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BIERMAN & MUSERLIAN
                                                                                                                                                                                                                           1131 CTCCTCCGATACCTGCTG 1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FELECOMMUNICATION INFORMATION TELEPHONE: (212) 661-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                  1 LeuLeuArgTyrLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.43e+06
6.00
                                                                                        100.00%
100.00%
0.86%
                                                         .23e+06
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100.00%
0.87%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: Unknown TOPOLOGY: Unknown
                                                                           6.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino Acid
                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
JS-09-419-826-39
                                                                                                                                                                                                                                                                                                                        US-08-244-951A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 39, Application US/09419826
Patent No. 6306832
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: FOR TREATING BREAST CANCER
NUMBER OF SEQUENCES: 99
COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
                                                                                                                                                                               APPLICANT: Seriero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REPERENCE: 29996.488 RDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
CURRENT APPLICATION NUMBER: US/08/991,862
CURRENT FILING DATE: 1998-08-17
EARLIER APPLICATION NUMBER: 08/863,862
EARLIER FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              used to raise the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide of mouse GP88 used to against the GP88 used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
         865 GACATGGAGGTGAGCTGCCCAGATGGCTATACC 897
                                                 5 AspMetGluValSerCysProAspGlyTyrThr 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-824-647-16 (1-2095) x US-08-991-862-5 (1-14)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/419,826
FILING DATE: 14-OCT-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/07711
FILING DATE: 14-APR-1998
APPLICATION NUMBER: US 60/043,545
FILING DATE: 14-APR-1997
INFORMATION FOR SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1). . (14)
OTHER INFORMATION: antisera against the
OTHER INFORMATION: immunoaffinity step.
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                                                                                                                        Sequence 5, Application US/08991862
Patent No. 6309826
GENERAL INFORMATION:
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100.00%
1.01%
                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: mouse granulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-419-826-39
                                                                                                      US-08-991-862-5
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                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.:
                                                                                      RESULT 5
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DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED PROTEIN TAU, HYBRIDOMAS SECRETING THESE ANTIBODIES, ANTIGEN RECOGNITION BY THESE MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
APPLICANT: VANMECHELEN, EUGEEN; VAN DE VOORDE, ANDRE
                                                      Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
                                                                             Mismatches:
                                                                                                                                                                                 US-09-824-647-16 (1-2095) x US-09-419-826-39 (1-8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: MONOCLONAL ANTIBODIES TITLE OF INVENTION: DIRECTED AGAINST THE NTITLE OF INVENTION: PROTEIN TAU, HYBRIDOM TITLE OF INVENTION: ANTIBODIES, ANTIGEN RE NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:
Length:
Matches:
                                                                                                             Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,951A
FILING DATE: 19-JAN-1995
CLASSIFICATION 435
PRIOR APPLICATION NUMBER: PCT/EP93/03499
FILING DATE: 10-DEC-1993
PRIOR APPLICATION UDERE: EP/92/403403.6
FILING DATE: 14-DEC-1992
APILING DATE: 14-DEC-1993
APILICATION NUMBER: EP/92/403403.6
FILING DATE: 14-DEC-1992
ATTORNEY/AGENT INFORMATION:
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US-08-934-222-113
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                                                                                                                            US-08-934-222-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
                                                                                                      RESULT 9
                                                                                                                                                                                                                                                                                    DIRECTED AGAINST THE MICROTUBBLE-ASSOCIATED PROFEIN TAU, HYBRIDOMAS SECRETING THESE ANTIBODIES, ANTIGEN RECOGNITION BY THESE MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS.
                                                                                                                                                                                                        Agtent NO. JOSTEL
GENERAL INFORMATION:
APPLICANT: VANDERMEREN, MARC; MERCKEN, MARC;
APPLICANT: VANMECHELEN, ENGEEN: VAN DE VOORDE,
APPLICANT: VANMECHELEN, ENGELONAL ANTIBODIES
MITTER OF INVENTION: MONOCLONAL ANTIBODIES

MITTER OF INVENTION: MONOCLONAL ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
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CIASSIPLCATION DATA:
APPLICATION NUMBER: 08/403,917
FILING DATE: 19-74N-1995.
PRIOR APPLICATION NUMBER: 08/403,916
FILING DATE: 19-13N-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/244,951
FILING DATE: 13-10N-1994
PRIOR APPLICATION NUMBER: 08/244,951
FILING DATE: 13-10N-1994
PRIOR APPLICATION NUMBER: 08/24,93403.6
FILING DATE: 10-DEC-1993
PRIOR APPLICATION NUMBER: EP/92/403403.6
FILING DATE: 14-DEC-1993
FILING DATE: 14-DEC-1993
FILING DATE: 14-DEC-1993
REGISTRATION NUMBER: 19,683
REGISTRATION NUMBER: 19,683
REGISTRATION NUMBER: 19,683
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 19,683
US-09-824-647-16 (1-2095) x US-08-244-951A-7 (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/389,011
FILING DATE: 15-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                             6 MUSERLIAN
                                                                                                                                                                   Sequence 5, Application US/08389011
Patent No. 5861257
                                         465 GGGCAGCACCCCCAGGA 448
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TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 5:
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0.87%
                                                                 600 THIRD AVENUE
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STRANDENNESS: Unknown
; TOPOLOGY: Unknown
US-08-389-011-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN
                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NEW YORK
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: NEW YORK
STATE: NEW YOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
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                                                                                                                                                      US-08-389-011-5
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Sequence 113, Application US/08934222
| Sequence 113, Application US/08934222 |
| Sequence 113, Application US/08934222 |
| Sequence 113, Application US/08934222 |
| Sequence 113, Application |
| Patent No. 5928896 |
| GENERAL INFORMATION: Constrainty |
| TITLE OF INVENTION: Polypeptides That Include Conformation |
| TITLE OF INVENTION: Constrainty Groups Which Flank A Protein Interact: |
| TITLE OF INVENTION: Site |
|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: TO LOUS, MAN DESCRIPTION BY SYSTEM: TO SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: US/08/934,222 APPLICATION NUMBER: US/08/934,222 FILING DATE: 19-SEPT-1997 PRIOR APPLICATION NUMBER: 08/532,818 FILING DATE: 03-MAY-1996 PRIOR APPLICATION DATA: US/08/143,364 APPLICATION NUMBER: U.S. 08/143,364 PRIOR APPLICATION DATA: APPLICATION NUMBER: U.S. 08/143,364 APPLICATION NUMBER: U.S. 08/143,364 APPLICATION NUMBER: U.S. 08/143,364 APPLICATION NUMBER: U.S. 08/051,741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
Mismatches:
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Matches:
US-09-824-647-16 (1-2095) x US-08-389-011-5 (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels:
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REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 113:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORIEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-933-402-113
; Sequence 113, Application US/08933402
; Patent No. 5948887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: EVANS, Herbert J.
                                                                                                 465 GGGGCAGCACCCCAGGA 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ProargGlyArgGlyMet
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Best Local Similarity:
Query Match:
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Sequence 113, Application US/08532818
Patent No. 5965698
GENERAL INFORMATION:
APPLICANT: EYANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Constraining Groups Which Flank A Protein Intera
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley, & Lardner
                              SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-824-647-16 (1-2095) x US-09-207-621-113 (1-9)
                                                                                   APPLICATION DATA:
PRIOR PAPELCATION BURS: US/09/207,621
FILING DATE:
APPLICATION NUMBER: US/09/207,621
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MX-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-GCT-1993
PRIOR APPLICATION DATA:
FILING DATE: 23-APR-1993
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels:
                                                                                                                                                                                                                                                                                                                                                                                          NAME: Isacson, John P.
REGISTATION'NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 113:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U.S. 08/143,364
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FILING DATE: 03-MAY-1996
PRIOR APPLICATION DAMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   270 CCCAGAGGCCGTGGCATG 287
             IBM PC compatible
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                                                                          DATA
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APPLICATION NUMBER:
                                                                     CURRENT APPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
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USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY:
US-09-207-621-113
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                                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
    KINI, R. Manjunatha
FENTION: Polypeptides That Include Conformation-
FENTION: Constraining Groups Which Flank A Protein-Protein Interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 113, Application US/09207621

Patent No. 5952465

CENERAL INFORMATION:
APPLICANT: ETANS, Herbert J.
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein Interaction
NUMBER OF SEQUENCES: 153

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,402
FILING DATE: 19-SEPT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 19-OST-1996
PRIOR APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,741
APPLICATION NUMBER: U.S. 08/051,741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
Mismatches:
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APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That In
TITLE OF INVENTION: Constraining Groups
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: ISACSOO, JOHN P.
RESISTANTION NUMBER: 33.751
REFERENCE PARKET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
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STREET: Suite 500, 3000 K (
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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COMPUTER READABLE FORM:
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SY: linear
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                            STATE: D
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: D
COUNTRY:
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Conservative: Mismatches: Indels:

Matches

Length:

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Proten-Protein Interacti
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/231,797
                                                                                                                                                                                                                                                                                                                                                                                                                US-09-824-647-16 (1-2095) x US-08-403-917A-5 (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: ISACSON, JOhn P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 113:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION DATE: 21-APK-12...
FILIDIA DATE: 21-APK-12...
APPLICATION NUMBER: U.S. 08/143,364
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FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 08/532,818
FILLING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILLING DATE: 21-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Sequence 113, Application US/09231797
Patent No. 6084066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     465 GGGCCACCCCCAGGA 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSEE: Foley & Lardner
F: Suite 500, 3000 K &
Washington
             TELECOMMUNICATION INFORMATION TELEPRA: (212) 661-8000 INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.43e + 06
                                                                                                                                                                                                                                                                                                               100.00%
REFERENCE/DOCKET NUMBER:
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APPLICATION NUMBER:
                                                                                                                                                                     STRANDEDNESS: Unknown TOPOLOGY: Unknown
                                                                                                                                                 Amino Acid
                                                                                                                                                                                                                                                                                                                                     Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                                 Percent Similarity
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                                                                                                                                                                                                            US-08-403-917A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
APPLICANT: VANDECHELEN, EUGEEN;
APPLICANT: VAN DE VOORDE, ANDE
TITLE OF INVENTION: MONOCILONAL ANTIBODIES
TITLE OF INVENTION: DIRECTED AGAINST THE MICK
TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SF
TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOCH
TITLE OF INVENTION: MONOCILONAL ANTIBODIES AND
                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
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APPLICATION NUMBER: 08/244,951
FILING BAPE: 13-UN-1994
FILING BAPE: 13-UN-1994
PRIOR APPLICATION DARA:
APPLICATION NUMBER: PCT/EP93/03499
FILING DARE: 10-DEC-1993
PRIOR APPLICATION DARA:
APPLICATION NUMBER: EP/92/403403.6
FILING DARE: 14-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAMME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels:
                                                                                                                      REFERENCE/DOCKET NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amain
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               FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: 08/256,167
FILING DATE: 27-JUN-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/08403917A Patent No. 6010913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    270 CCCAGAGGCCGTGGCATG 287
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                                                                                                                                                                                                                                                                                                                                                         6.43e+06
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
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STATE: NEW YORK
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Best Local Similarity:
Query Match:
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US-08-403-917A-5
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Street NW

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Sequence 113, Application US/08934223
Patent No. 6147189
GENERAL INFORMATION:
APPLICANT: EYANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Solstraining Groups Which Flank A Protein Intera
                                                                                                                                                          APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interi
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
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Indels:
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Matches:
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APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,843
FILING DATE: 19-SEPT-1997
PRIOR APPLICATION DATA:
                                                                                                   Sequence 113, Application US/08933843 Patent No. 6111069 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/532,818 FILING DATE: 03-MAY-1996
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STREET: Suite 500, 3000 K :
CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEC ID NO:
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APPLICATION NUMBER:
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Query Match:
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STATE:
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                                                                                                                                                                                                                                                                                                            Sequence 113, Application US/08934224
Patent No. 610044
GENERAL INFORMATION:
APPLICANT: EYANS, Herbert J.
APPLICANT: EVANS, Herbert J.
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein Interaction
TITLE OF INVENTION: Site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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Mismatches:
                                                              Conservative Mismatches:
                                                                                                                                                        US-09-824-647-16 (1-2095) x US-09-231-797-113 (1-9)
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                      Length:
Matches:
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Matches:
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APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION NUMBER: U.S. 08/051,741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: ISSESS
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Suite 500, 3000 K Street NW
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                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
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                                                    Percent Similarity:
Best Local Similarity:
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Alignment Scores
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DB:
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                  Pred. No.:
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: VANDERNEEREN, MARC; MERCKEN, MARC;
APPLICANT: VANDERNEEREN, BUGEEN;
APPLICANT: VAN DE VOORDE, ANDRE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATION
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,223
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Mismatches:
Indels:
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Matches:
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APPLICATION NUMBER: US/08/532,818
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
FILING DATE: 21-APR-1994
FILING DATE: 29-0CT-1993
FILING DATE: 29-0CT-1993
PRIOR APPLICATION DATA:
FILING DATE: 23-APR-1993
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: ISACSON, JOHN P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 113:
                                      CORRESPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
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CITY: NEW YORK
STATE: NEW YORK
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0.86%
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MEDIUM TYPE: Floppy disk
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                            NUMBER OF SEQUENCES:
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GY: linear
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Best Local Similarity:
Query Match:
                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-934-223-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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US-09-348-952A-5
                                                                                                                                                              20007
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Sequence 113, Application US/09413492

Patent No. 6258550

GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: EVANS, Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interactive of INVENTION: Site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-824-647-16 (1-2095) x US-09-348-952A-5 (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08,403,917
FILING DATE: 19-JAN-1995
APPLICATION NUMBER: 08,256,167
FILING DATE: 27-JUN-1994
PRIOR APPLICATION NUMBER: 08,244,951
FILING DATE: 13-JUN-1994
PRIOR APPLICATION NUMBER: 08,244,951
FILING DATE: 10-DEC-1993
PRIOR APPLICATION NUMBER: PCT/FP93/03499
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA: PCT/FP93/03499
FILING DATE: 14-DEC-1993
ATORNEY/AGENT INFORMATION:
NAME: CHARLES A. WORSERIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 19,683
TELLCOMMUNICATION:
TELLCOMMUNICATION:
                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/348,952A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    465 GGGCAGCACCCCAGGA 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Foley & Lardner STREET: Suite 500, 3000 K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8000
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.43e+06
6.00
100.00%
100.00%
0.87%
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: Amino Acid
STRANDEDNESS: Unl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
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E: PANITCH SCHWARZE JACOBS & NADEL, P.C. ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND FL.
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APPLICANT: DOMBROSKI, BETH A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF
TITLE OF INVENTION: MAMMALIAN RETROTRANSPOSONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/847,844A
FILING DATE: 28 APR-1997
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
Mismatches:
                                                                                                                  RESULT 21
5470825-3
;Patent No. 5470825
;WILDE, CRAIG G.
TITLE OF INVENTION: BASOPHIL GRANULE PROTEINS
; NUMBER OF SEQUENCES: 8
       US-09-824-647-16 (1-2095) x US-09-053-611-6 (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches:
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                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,564
FILING DATE: 15-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 551,263
FILING DATE: 10-JUL-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/749,805
FILING DATE: 16-NOV-1996
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-847-844A-80; Sequence 80, Application US/08847844A; Patent No. 6150160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KAZAZIAN JR., HAIG H.
BOEKE, JEF D.
MORAN, JOHN V.
                                              1131 CTCCTCCGATACCTGCTG 1148
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                                                                                 1 LeuLeuArgTyrLeuLeu 6
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COMPUTER READABLE FORM:
MEDIUM TYPE: Flore
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.:
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APPLICANT: Hart, Charles P.
APPLICANT: Schatz, Peter J.
APPLICANT: Glaxo Group Limited
TITLE OF INVENTION: Compositions and Methods for Detecting Ligand Dependent
TITLE OF INVENTION: Nuclear Receptor and Coactivator Interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence:LCD (leucine OTHER INFORMATION: charged domain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  00000
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SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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Mismatches:
Indels:
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Indels:
Gaps:
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Matches:
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CURRENT APPLICATION NUMBER: US/09/053, 611
CURRENT FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 40
                                                                                                                                                                                                                                          APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-ARR-1993
ATONNEY/AGENT INFORMATION:
NAME: ISAGSON, JOHN P.
                                                                                                                                                                                  APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
                                                                                                                                 APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
                                    APPLICATION NUMBER: US/09/413,492
                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/09053611
Patent No. 6410245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             270 CCCAGAGGCCGTGGCATG 287
                                                                                                                                                                                                                                                                                                 NAME: Isacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 04
                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 113: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 6
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
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100.00%
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                                                                                                                                                                                                                                                                                                                                                                                                  9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
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                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-413-492-113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.:
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Cerottini, Jean-Charles

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Milbrandt, Jeffrey D.
APPLICANT: Milbrandt, Jeffrey D.
APPLICANT: Milbrandt, Jeffrey D.
TITLE OF INVENTION: Artemin, A No. 6284540el Neurotrophic Factor
TITLE OF INVENTION: Artemin, A No. 6284540el Neurotrophic Factor
FILE REFERENCE: 6029-7998
CURRENT FILING DATE: 1988-12-24
CURRENT FILING DATE: 1998-12-22
EARLIER APPLICATION NUMBER: 60/218,698
EARLIER FILING DATE: 1998-11-12
EARLIER FILING DATE: 1998-11-12
EARLIER FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 120
SOFTWARE: PATENTIN VET: 2.0
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Matches:
Conservative:
Mismatches:
Indels:
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Mismatches:
Indels:
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Matches:
                  9596-2302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 27, Application US/09099543C
Patent No. 6326200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 91, Application US/09220528A Patent No. 6284540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1325 ACCCCAGAGACATCGGCT 1342
                                                                                                                                                                                                                                                                                                                                                                                            1164 GGAGTGGGGCTGCTGTCC 1181
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                                                                                                                                                                                                                                                                                                                                                                                                             4 GlyValGlyLeuLeuSer 9
     36,317
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6.00
100.00%
100.00%
0.86%
REGISTRATION NUMBER: 36,31
REFERENCE/DOCKET NUMBER: 9:
TELECOMMUNICATION INFORMATION
TELEPHONE: 215-567-2020
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6.00
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100.00%
0.86%
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                                                                                                                   10 amino acids
                                                                     TELEFAX: 215-567-2991
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                215-567-2991
                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                               TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                 US-08-847-844A-80
                                                                                                                                                                                                                                   Alignment Scores:
Pred. No.:
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.09-220-528-91
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LENGTH: 10
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DISORDERS, OR DISEASES INVOLVING
TITLE OF INVENTION: Isolated No. 6326200a - And Decapeptides Which Bind TITLE OF INVENTION: TO HLA Molecules, and the Use Thereof FILE REFERENCE: LUD 5483.2 CURRENT APPLICATION NUMBER: US/09/099,543C CURRENT FILING DATE: 1998-06-18
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Mismatches:
Indels:
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: LO, CONTINUED APPLICANT: LO, CONTINUED APPLICANT: Thomas, Mary Beth APPLICANT: Thomas, Mary Beth APPLICANT: PUTCHORY, Stuart D. APPLICANT: PUTCHORY, CASTURIA APPLICANT: Ratz, Lawrence C. TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: COMPOSITIONS AND TREATING CONDITIONS, DISTILE OF INVENTION: CELL DEATH TITLE OF INVENTION: CELL DEATH TITLE OF ENVENTION: CELL DEATH CURRENT FILING DATE: 1999-12-14

NUMBER OF SEQ ID NOS: 466

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 11
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                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels:
                                                                                            PRIOR APPLICATION NUMBER: US 09/061,388 PRIOR FILING DATE: 1998-04-16 PRIOR RAPLICATION NUMBER: US 08/880,963 NUMBER OF SEQ ID NOS: 32 SEQ ID NO 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: Lo, Donald C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-461-697-66
; Sequence 66, Application US/09461697
; Patent No. 6277974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1311 GCGGCGGCCAGGCATCTT 1294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     903 GCAGCAGGTATAGCCATC 886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.28e+03
6.00
100.00%
100.00%
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                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                    5.37e+03
                                                                                                                                                                                                                                                                                                                                                                                                         100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GRGANISM: Homo sapiens US-09-461-697-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                          Aliqnment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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Q
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Sequence 19,

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MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,306A
FILING DATE: 02-0ct-1996
                                                                                                                     FILING DATE: 02-0ct-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 95/20080.4
FILING DATE: 02-0ct-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/009,832
FILING DATE: 01-03n-1996
ATTORNEY/AGEWT INFORMATION:
NAME: Williams, Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380
REFERENCE/POCKET NUMBER: 96,048-A (3255/00784)
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-824-647-16 (1-2095) x US-08-726-306A-161 (1-13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/602,999A
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Patent No. 6184205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1663 AGACGCCCTGGGCGTAGG 1646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 ArgArgProGlyArgArg 9
                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (617) 345-9111
INFORMATION FOR SEQ ID NO: 16
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.15e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.00%
100.00%
0.87%
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APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ercent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-602-999A-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏ
                                                                                                                         JACKSEE: Flehr, Hohbach, Test, Albritton & Herbert STREET: Fubarcadero Center, Suite 3400 CITY: San Francisco STATE: California COUNTRY: United 1
                                                                                                                                                                                                                                                                                             COMPUTER READDALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,850
FILING DATE: 24-JUL-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: van Leeuwen, Frederik Willem
APPLICANT: Burbach, Johannes Peter Henri
APPLICANT: Grosveld, Franklin G.
ATTLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS
NUMBER OF SEQUENCES: 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-824-647-16 (1-2095) x US-08-672-850-19 (1-12)
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Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPERENCE/DOCKET NUMBER: A 63610
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3349
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 1 Financial Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 161, Application US/08726306A
Patent No. 5958684
GENERAL INFORMATION:
                                  Sequence 19, Application US/08672850
Patent No. 6140117
                                                                       GENERAL INFORMATION:
APPLICANT: Milbrandt, Jeffrey
APPLICANT: Arail, Toshiyuki
TITLE OF INVENTION: INJURIN
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: S11va, Robin M.
REGISTRATION NUMBER: 38,304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.21e+03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                 94111
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                     US-08-672-850-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-672-850-19
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unknown
amino acid
                                                                                                                                               Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                        Alignment Scores:
                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
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                                                                                                                                                                                   Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.:
                                                                                                               Pred. No.:
                                                                                                                                  Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Src SH3 BINDING PEPTIDES AND METHODS OF TITLE OF INVENTION: ISOLATING AND USING SAME NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/278,865
                                                                                                                                                                                                                                                                                                                                                                                                Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-824-647-16 (1-2095) x US-08-602-999A-82 (1-13)
                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Villacorta, Gilberto M.
REGISTRATION NUMBER: 34,038
REFRENCE/DOCKET NUMBER: 4980-007-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . Sequence 82, Application US/08278865
. Patent No. 6303574
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: KAY, BRIAN K.
APPLICANT: SPARKS, ANDREW B.
APPLICANT: THORN, JUDITH M.
APPLICANT: QUILLIAM, LAWRENCE A.
APPLICANT: DER, CHANNING J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1513 AGACCACTTCCTTCGC 1496
                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFRERENCE/POCKET NUMBER: 1101
TELECOMMUNICATION INFORMATION:
                                                                                                                                         TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ. ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
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6.00
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100.00%
0.87%
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                16-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: peptide
US-08-602-999A-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    virginia
: U.S.A.
                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                           unknowr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22202
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ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                      Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 29
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:No. 6423680el sequence
US-09-183-841-4
                                                                                                                                                                                                                                                                   Sequence 4, Application US/09183841

Sequence 4, Application US/09183841

Patent No. 6423680

GENERAL INFORMATION:

APPLICANT: Hospital for Sick Children

TITLE OF INVENTION:

FILE REFERENCE: vanc0010

CURRENT APPLICATION NUMBER: US/09/183,841

CURRENT FILING DATE: 1998-10-30

NUMBER OF SEQ ID NOS: 4

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 4

LENGTH: 13
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0000
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Mismatches:
Indels:
                                                                                          Conservative:
Mismatches:
Indels:
                                                                                                                                                                       US-09-824-647-16 (1-2095) x US-08-278-865-82 (1-13)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
                                                                                 Matches:
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STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 82, Application US/09500124 Patent No. 6432920 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QUILLIAM, Lawrence A. DER, Channing J. FOWLKES, Dana M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          680 AGCTGCCCAGTGGGAAGT 697
                                                                                                                                                                                                         1513 AGACCACTTCCTTCTCGC 1496
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THORN, Judith M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.15e+03
6.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIDER, James E.
                                                                                                                                                                                                                       4 ArgProLeuProSerArg
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100.00%
0.86%
                                                                5.15e+03
                                                                                            100.00%
100.00%
0.87%
MOLECULE TYPE: peptide US-08-278-865-82
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Best Local Similarity:
Query Match:
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Sequence 120, Application US/08445745
Patent No. 5672585
GENERAL INFORMATION:
APPLICANT: Pierschbacher, Michael D.
APPLICANT: Cheng, Soan
APPLICANT: Craig, William S.
APPLICANT: Tschopp, Juerg F.
TITLE OF INVENTION: Methods and Composition for Treating
TITLE OF INVENTION: Thrombosis
NUMBER OF SEQUENCES: 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/445,745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-824-647-16 (1-2095) x US-08-766-596A-40 (1-13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels:
                                                                                                                                                REFERENCE/DOCKET NUMBER: SOTO-JARA-1A TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197 TELEPEAX: 202-737-3528 INFORMATION FÓR SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/050,73614

TITTING DATE: 14-APR-1993
                FILING DATE: 10-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION DATA:
APPLICATION NUMBER: US 08/171,068
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: US 08/079,441
FILING DATE: 18-JUN-1993
us 08/630,645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1631 GCTGGGCCTGCTGTCCCT 1648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 AlaGlyProAlaValPro 12
                                                                                                                  NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
              10-APR-1996
                                                                         FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              15e+03
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                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1(CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Campbell
STREET: 4370 La Jol
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: S1
                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                    US-08-766-596A-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-445-745-120
                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: BAUMANN, MAIC

PEPLICANT: FRANKIONE, BLAS

TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES

TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES

TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE

TITLE OF INVENTION: DEPOSITS

NUMBER OF SEQUENCES: 69
                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3: BROWDY AND NEIMARK
419 Seventh Street, N.W., Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-824-647-16 (1-2095) x US-09-500-124-82 (1-13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,596A
                                                                                                                               APPLICATION NUMBER: US/09/500,124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 6462171
GENERAL INFORMATION:
APPLICANT: SOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1513 AGACCACTTCCTTCGC 1496
                                                                                                                                                                                                                                                                                                                                                      (212) 790-9090
(212) 869-9741/8864
                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                           NAME: Misrock, S. Leslie
REGISTATION NUMBER: 18/872
REFERENCE/DOCKET NUMBER: 11
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 82:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 ArgProLeuProSerArg
    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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100.00%
0.87%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / MOLECULE TYPE: peptide US-09-500-124-82
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COMPUTER READABLE FORM:
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ADDRESSEE: BROWDY AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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Best Local Similarity:
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                                                                                                                                                      FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
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US-09-824-647-16 (1-2095) x US-09-120-365-84 (1-14)
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                                                       APPLICANT: Natori, Shunji
TITLE OF INVENTION: NEW PROTEASE
FILE REFERENCE: 32290-14419.
CURRENT APPLICATION NUMBER: US/09/120,365
CURRENT FILING DATE: 1998-07-22
EARLIER APPLICATION NUMBER: JP 9-333 474
EARLIER FILING DATE: 1997-11-18
NUMBER OF SEO ID NOS: 101
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Natori, Shunji
TITLE OF INUENTION: NEW PROTEASE
FILE REFERENCE: 32290-144749
CURRENT APPLICATION NUMBER: US/09/120,365
CURRENT FILING DATE: 1998-07-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 86, Application US/09120365 Patent No. 6103514 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 84, Application US/09120365
Patent No. 6103514
Sequence 83, Application US/09120365
Patent No. 6103514
GENERAL INFORMATION:
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TITLE OF INVENTION: NEW PROTEASE
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EARLIER FILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 101
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 84
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Best Local Similarity:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: bovine
                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: rattus
US-09-120-365-83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
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TYPE: PRT
                                                                                                                                                                                                                                                         SEQ ID NO 83
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                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.:
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Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
Indels:
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TITLE OF INVENTION: NEW PROTEASE
FILE REFERENCE: 32290-144749
CURRENT APPLICATION NUMBER: US/09/120,365
CURRENT FILING DATE: 1998-07-22
REALIER APPLICATION NUMBER: JP 9-333 474
RALLIER FILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 101
SOFTWARE: Patentin Ver: 2.0
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                 APPLICATION NUMBER: US 07/681,119
FILING DATE: 05-APR-1991
PRIOR APPLICATION DATE: ...
APPLICATION NUMBER: US 07/506,444
FILING DATE: 06-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFRENCE/DOCKET NUMBER: P-LA 9829
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 82, Application US/09120365
Patent No. 6103514
GENERAL INFORMATION:
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                      amino acid
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Best Local Similarity:
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US-09-120-365-82

RESULT 34

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Conservative: Mismatches:

Indels:

Alignment Scores:

Score:

Query Match:

Matches:

Length:

400000

Conservative: Mismatches: Indels:

RESULT 35 US-09-120-365-83

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Alignment Scores:

US-09-120-365-82

SEQ ID NO 82 LENGTH: 14

Matches:

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Score:
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Matches:
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                                                                                                                                                                                                                                                                                                                                 Indels:
FILE REFERENCE: 32290-144749
CURRENT APPLICATION NUMBER: US/09/120,365
CURRENT FILING DATE: 1998-07-22
EARLIER APPLICATION NUMBER: 1P 9-333 474
EARLIER FILING DATE: 1997-11-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 32290-144749
CURRENT APPLICATION NUMBER: US/09/515,039
CURRENT FILING DATE: 2000-03-06
EARLIER FILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 101
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CURRENT FILING DATE: 2000-03-06
EARLIER APPLICATION NUMBER: JP 9-333 474
EARLIER FILING DATE: 1997-11-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 83, Application US/09515039
Patent No. 6214599
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 82, Application US/09515039
Patent No. 6214599
                                                                                                                                                                                                                                                                                                                                                                                                                          1270 AGCGAGATCGTGGCTGGA 1287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Natori, Shunji
TITLE OF INVENTION: NEW PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 SerGlulleValAlaGly 11
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TITLE OF INVENTION: NEW PROTEASE
FILE REFERENCE: 32290-144749
                                                                                                                                                                                                                                                                                                                                                                                                                                             6 SerGlulleValAlaGly 11
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100.00%
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                                                                                          NUMBER OF SEQ ID NOS: 101
SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
Query Match:
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                                                                                                                                                                ; TYPE: PRT
; ORGANISM: chicken
US-09-120-365-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; .ORGANISM: murine US-09-515-039-82
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                                                                                                                              SEQ ID NO 86
                                                                                                                                                   LENGTH: 14
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TITLE OF INVENTION: NEW PROTEASE
FILE REFERENCE: 32290-144749
CURRENT APPLICATION NUMBER: US/09/515,039
CURRENT FILING DATE: 2000-03-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/515,039 CURRENT FILING DATE: 2000-03-06
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Patent No. 6214599
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TITLE OF INVENTION: NEW PROTEASE
FILE REFERENCE: 32290-144749
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EARLIER FILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 101
SOFTWARE: PATENTIN VET. 2.0
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EARLIER FILING DATE: 1997-11-18
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 84
LENGTH: 14
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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                                             ; ORGANISM: rattus US-09-515-039-83
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US-09-515-039-86
SEQ ID NO 83
LENGTH: 14
                                 TYPE: PRT
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ORGANISM: Artificial Sequence
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TITLE OF INVENTION: Interaction Between Cyclin D1 and Steroid Receptor
TITLE OF INVENTION: Co-Activators and Uses Thereof in Assays
FILE REFERENCE: 4238/80713
CURRENT APPLICATION NUMBER: US/09/302,305C
CURRENT FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: PUT/GB99/00440
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Kim, Seong-Tae
APPLICANT: Kim, Seong-Tae
APPLICANT: Lim, Dae-Sik
APPLICANT: Lim, Dae-Sik
APPLICANT: St. Jude Children's Research Hospital
ATITLE OF INVENTION: ATM Kinase Modulation for Screening and Therapies
FILE REPERENCE: 2427/1F142
CURRENT APPLICATION NUMBER: US/09/400,653A
CURRENT FILING DATE: 1999-09-21
PRIOR APPLICATION NUMBER: 09/248,061
PRIOR FILING DATE: 1999-02-10
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Matches:
Conservative:
Mismatches:
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Mismatches:
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Matches:
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Sequence 11, Application US/09400653A
Patent No. 6348311
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APPLICANT: Kastan, Michael
APPLICANT: Canman, Christine
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SOFTWARE: Patentin Ver. 2.1
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APPLICANT: Bernards, Rene
APPLICANT: Zwijsen, Renat
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SOFTWARE: FastSEQ for
SEQ ID NO 11
LENGTH: 14
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
; ORGANISM: chicken US-09-515-039-86
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                                                    Alignment Scores:
Pred. No.:
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APPLICANT: Kastan, M.
APPLICANT: Canman, C.
APPLICANT: Kim, S-T.
APPLICANT: Kim, S-T.
APPLICANT: St. Jude Children's Research Hospital
TITLE OF INVENTION: ATM Kinase Modulation for Screening and Theraples
FILE REFERENCE: 2427/OF142
CURRENT APPLICATION NUMBER: US/09/248,061B
CURRENT FILING DATE: 1999-02-10
NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and Steroid Receptor
                                                                                         181
OTHER INFORMATION: Description of Artificial Sequence: Peptide OTHER INFORMATION: containing an LAXLL motif found in steroid oTHER INFORMATION: receptor coactivators
US-09-302-305C-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bernards, Rene
APPLICANT: Zwijsen, Renate
TITLE OF INVENTION: Interaction Between Cyclin D1 and Steroid
TITLE OF INVENTION: Co-Activators and Uses Thereof in Assays
FILE REFERENCE: 4238/80713
CURRENT APPLICATION NUMBER: US/09/302,305C
CURRENT FILING DATE: 1999-04-30
PRIOR APPLICATION UNDER: PCT/GB99/00440
PRIOR APPLICATION UNDER: PCT/GB99/00440
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
LENGTH: 14
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APPLICANT: Kastan,
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Query Match:
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FastSEQ for Windows Version 3.0
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                                            ; ORGANISM: Homo Sapiens
US-09-248-061B-9
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Best Local Similarity: 1
Query Match:
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Pred. No.:
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US-09-824-647-16 (1-2095) x US-09-248-061B-9 (1-14)

Search completed: July 7, 2003, 16:09:34 Job time: 33 secs

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GERERAL INFORMATION:
APPLICANT: SETECTO, GINETLE
APPLICANT: SETECTO, GINETLE
APPLICANT: SETECTO, GINETLE
APPLICANT: SOFTING TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REPERENCE: 29996.488/P001-A
CURRENT APPLICATION NUMBER: US/08/991,862
CURRENT FILING DATE: 1999-08-17
EARLIER FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PALENTIN Ver: 2.0
SEQ ID NO 17
                                                                                                                                              Sequence 8, Sequence 7, Sequence 2, Sequence 2, Patent No. 54
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                     PCT-US91-02321-6
US-08-991-862-6
US-07-668-648-8
US-08-429-998-8
US-08-431-333-8
PCT-US91-02321-8
US-08-991-862-7
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US-09-060-756-732
US-08-584-031-11
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US-09-372-422A-26
US-09-282-305-14
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US-09-216-386-3
US-09-216-386-5
US-08-878-862-3
US-09-213-394-3
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US-08-446-922-8
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US-09-022-940-3
US-09-022-940-5
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US-09-391-958-1
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US-08-573-675-2
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Patent No. 6309826
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-Q-Q0012_1702PO_29009246477runat_07072003_154719_26078/app_query.fasta_1.2247
-Q0012_1702PO_29009246477_cata_ -SUFFIX-setd_rai -MINMATCH-0.1 -LOOPCIL-0
-LOOPEXT-0 -UNITS-bits -START-1 -END--1 -MATRIX-oligo -TRANS-human40.cdi
-LIST-45 -DOCALIGN-00 -THEAPSTIZE-500 -MATRIX-NOTO0000000
-USFR-US09824647_CGCN_1 1_33_erunat_07072003_154719_26078 -NCPU-6 -ICPU-3
-NO_MARP -LARGEQUER NEG_SCORES-0 -WAIT -DSPELOCK-100 -LONGLOG
-PSTARN-TIMEOUT-30 -THERAPS-1 -XGAPOP-66 -XGAPEXT-60 -FGAPOP-6
-FGAPORT-7 -YGAPOP-60 -YGAPEXT-60 -DELOP-6 -DELEXT-7
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/cgn2_6/ptodata/1/laa/6A_COMB.pep:*
/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
                          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                            - protein search, using frame_plus_n2p model
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US-07-668-648-4
US-08-429-998-4
US-08-431-333-4
PCT-US91-02321-4
US-07-668-648-2
US-08-429-998-6
US-08-429-998-6
US-08-431-333-2
US-08-431-333-2
US-08-431-333-2
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Maximum DB seq length: 200000000
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Ωp	21 ProAspGlyGlnPheCysProValAlaCysCysLeuAspProGlyGlyAlaSerTyrSer 40	2222542542424242425425425425425425425425
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Oy D	253 TCCAGTTGCTGCCCTTCCCAGAGGCCGTGGCATGCGGGGATGGCCATCACTGCTGCCCA 312	1333
\$ g	313 CGGGGTTCCACTGCAGTGCAGAGGGTGTCCTGCTTCCAAAGATCAGGTAACAACTCC 372 	1393
. qg	373 GTGGGTGCCAGTGCCCTGATAGTCAGTTCGAATGCCCGGACTTCTCCACGTGCTGT 432. 	481
ζ, 6	433 GTTATGGTCGATGGCTCCTGGGGGTGCTGCCCCAGGCTTCCTGCTGAAGAC 492 	501
ζς 2Ω	493 AGGGGCACTGCTGCCGACGGTGCCTTCTGCGACCTGGTTCACACCCGCTGCATCACA 552 	15/3
ý d	553 CCCACGGGCACCCCCCCGGCAAAGAAGCTCCCTGCCCAGAGGACTAACAGGGCAGTG 612 	1633
oy Q	613 GCCTTGTCCAGCTCGGTCATGTGTCCGGACGCACGGTCCCGGTGCCCTGATGGTTCTACC 672 [561
& B	673 TGCTGTGAGCTGCCCAGTGGGAAGTATGGCTGCCGAATGCCCAACGCCACCTGCTGC 732 	Oy 1753 GACGCCCTTTGAGG
. Q	733 TCCGATCACCTGCACTGCCCCCAAGACACTGTGTGACCTGATCCAGAGTAAGTGC 792 	RESULT 2 US-007-668-648-4 ; Sequence 4, Application US/U ; Patent No. 5416192.
Vo Qa	793 CTCTCCAAGGAGAACGCTACCACGGACCTCCTCACTAAGCTGCCCACCACAGTGGGC 852 	; GEMERAL INFORMATION: ; GAPLICANT: Shoyab, Mohan ; APPLICANT: Plowman, Gree ; TITLE OF INVENTION: EPTI
Oy Og	853 GATGTGAAATGTGACATGGAGGTGAGCTGCCCAGATGGCTATACCTGCTGCTGCTACAGG 912 	; TITLE OF INVESTES: 12 CORRESPONDENCE ADDRESS: 12 CORRESPONDENCE ADDRESS: ; ADDRESSEE: Pennie 6 E
yo g	913 TCGGGGCCTGGGGCTGCTGTTTACCCAGCTGTGCTGTGAGGACCACATACAC 972 	ET: LISS Avenue : New York E: New York IRY: USA
Oy Q	973 TGCTGTCCCCGCGGGTTTACGTGTGACACGCAGAAGGGTACCTGTGAACAGGGGCCCCCAC 1032 	O 144
oy op	1033 CAGGTGCCCTGGATGGAGAAGGCCCCAGCTCACCTGCCAGACCCACAAGCCTTG 1092 	CUPERATING STATEM: SOFTWARE: Patentin Re- CURRENT APPLICATION DATA APPLICATION NUMBER: US
Oy Op	1093 AAGAGAGATGTCCCCTGTGATAATGTCAGCTGTCCTCCTCCGATACCTGCTGCCGA 1152 	FILING DALE: 1991019; CLASSIFICATION: 514 ; ATTORNEY/AGENT INFORMATION: MANE: Misrock, S. Les,
Oy Op	1153 CTCACGTCTGGGGAGTGGGGCTGCTGTCCAGAGGCTGTCTGCTGCTGGACCAC 1212 	REGLETARATION NUMBER: REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORM: TELEPHONE: (212)790-99

CCACCGATACACGTCTGACCGACGCAGTGTCACCGAGGAGC 1272 CHACGCCCAGGGCGTCTGTTGTGCTGATCGGCGCCCACTGCTGTCCT 1692 CACCTTCCTGGCCCGTAGCCCTCACGTGGGTGTGAAGGACGTGGAG 1572 CAGCACACCAGCTGCCCGGTGGGCGGAACCTGCTGCCCGAGCCAG 1392 THECTECCAGTTECCCCATECTGTGTGCGAGGATCGCCAGCAC 1452 200 egory D. ITHELINS: NOVEL CYSTEINE-RICH GROWTH DULATING PROTEINS SGACCCAGCCTTGAGACAGCTGCTG 1791 gAspProAlaLeuArgGlnLeuLeu 593 elease #1.0, Version #1.25 eslie 18,872 BER: 5624-161-999 RRMATION: -9090 Edmonds of the Americas A: US/07/668,648 -DOS/MS-DOS /07668648 patible ION:

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                               GATGTGAAATGTGACATGGAGGTGAGCTCCCCAGATGGCTATACCTGCTGCTGCTCTACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CY
TITLE OF INVENTION: MODULATING PROTEINS
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MEDIUM TYPE: Floppy disk
COMPUTER: TIBM PC compatible
COMPUTER: TIBM PC compatible
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Vei
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,998
FILING DATE: 27-APR-1995
CLASSIFICATION: 514
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                             1213 CAGCACTGCTCCCCCAG 1230
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08429998 Patent No. 5885961
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TELECOMMUNICATION INFORMATION:
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(212) 869-9741
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & 1
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                             Indels:
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100.00%
100.00%
58.50%
TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 593 amino acids
TYPE: AMINO ACID
                                                                                MOLECULE TYPE: protein
                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                      Alignment Scores:
Pred. No.:
                                                                 TOPOLOGY:
                                                                                            US-07-668-648-4
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DB: .
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Db 301 S		Db 321 c	Qy . 1033 C	Db 341 G	Qy 1093 A	Db 361 I	0y 1153 C	Db 381 I	0y 1213 C	DD 401 C	RESULT 4	US-08-431-333-4 ; Sequence 4, 7 ; Patent No. 59				CORRESPON			COUNTRY SIP: 10	COMPUTER	COMPUTE	SOFTWAR	; APPLICA	CLASSIF	APPLICA	ATTORNEY	REGISTR	TELECOMMU	; TELEFAX	SEQUENCE	TYPE:	; MOLECULE US-08-431-333-	Aliqument Scor	Pred. No.: Score:	Percent Simila Best Local Sim	Query Match: DB:
	ment Scores: 0	is 406.00 Matches: ont Similarity: 100.00% Conservative:	Local Similarity: 100.00% Match: 58.50%	Gaps: 	()		しからしましてもしてもしていることには、 このでは、 この	CCA6ATGGTCAGTTCTGCCCTGTGGCCTGCTGGAGCCCCGGAGGAGCAGCTACTGCTGCTGGAGCAGCAGCTACTGCTGCTGCTGCTGCTGGAGCAGCAGCAGCAGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGC	Proasperyellynecyskrovalatacyscysbemssprroeryatyaraseriytoer	TGCTGCCGTCCCCTTCTGGACAATGGCCCACAACACTGAGCAGGCATCTGGGTGGCCCCC	_	193 TGCCAGGTTGATGCCCACTGCTCTGCGGCCACTCTGCATCTTTACCGTCTCAGGGACT 252	できならまして ロードン プロ・ドラー コード・ドゥー・ドゥー・ドゥー・ドゥー・ドゥー・ドゥー・ドゥー・ドゥー・ドゥー・ド		SerSerCysCysProPneProGlualaValAlaCysGlyAsPolyHisHisCysCysPro	CGGGGCTTCCACTGCAGTGCAGTGCAGCGCGATCCTGCTTCCAAAGATCAGGTAACAACTCC	101 ArgGlyPheHisCysSerAlaAspGlyArgSerCysPheGlnArgSerGlyAsnAsnSer 120	373 GIGGGIGCCATCCAGIGCCCIGATAGICAGITCGAAIGCCCGGACIICTCTCCACGIGCIGT 432	121 ValGlyAlaileGinCysProAspSerGinPheGluCysProAspPheSerThrCysCys 140	433 GTIAIGGICGAIGGCICCTGGGGGGGGCTGCCCCAGGCIICCTGCTGTGAAGAC 492	141 ValMetValAspGlySerTrpGlyCysCysProMetProGlnAlaSerCysCysGluAsp 160	493 AGGGACTGCTGTCCGCACGGTCCTTCTGCGACCTGGTTCACACCCGCTGCATCACA 552	161 ArgvalHisCysCysProHisGlyAlaPheCysAspLeuValHisThrArgCysIleThr 180	553 CCCACGGGCACCCACCCCTGGCAAGAAGCTCCCTGCCCAGAGGACTAACAGGGCAGTG 612	181 ProThrGlyThrHisProLeuAlaLysLysLeuProAlaGlnArgThrAsnArgAlaVal 200	613 GCCTTGTCCAGCTCGGTCATGTGTCCGGACGCACGGTCCCGGTGCCCTGATGGTTCTACC 672	201 AlaLeuSerSerSerValMetCysProAspAlaArgSerArgCysProAspGlySerThr 220	673 TGCTGTGAGCTGCCCAGTGGGAAGTATGGCTGCTGCCCAATGCCCAACGCCACTGCTGC 732	221 CysCysGluLeuProSerGlyLysTyrGlyCysCysProMetProAsnAlaThrCysCys 240	733 TCCGATCACCTGCACTGCTGCCCCCAAGACACTGTGTGTG	241 SerAspHisLeuHisCysCysProGlnAspThrValCysAspLeulleGlnSerLysCys 260	793 CICICCAAGGAACGCIACCACGGACCICCTCACIAAGCIGCCGCGCACACACAGGGGC 852	261 LeuSerLysGluAsnAlaThrThrAspLeuLeuThrLysLeuProAlaHisThrValGly 280	853 GAIGTGAAATGTGACATGGAGGTGAGCTGCCCAGATGGCTATACCTGCTGCCGCTCTACAG 912		913 TCGGGGCCTGGGGCTGCTGCTTTTACCCAGGCTGTGTGCTGTGAGGACCATACAC 972
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T: Shoyab, Mohammed
T: Shoyab, Mohammed
T: Plowman, Gregory D.
INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
INVENTION: DOULATING PROTEINS
F SEQUENCES: 12
NDENCE ADDRESS:
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IUM TYPE: Floppy disk

PUTER: IBM PC compatible

PUTER: IBM PC compatible

PUTER: PATENT SYSTEM: PC-DOS/MS-DOS

TWARE: PATENT SISPEM: PC-DOS/MS-DOS

TWARE: PATENT SOS SISPEM: US/08/431,333

LICATION NUMBER: US/08/431,333

SSIFICATION: 536

APPLICATION: 536

APPLICATION NUMBER: US 07/668,648

ING DATE: 13-MAR-1991

ING DATE: INS-MAR-1991

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RENCE/DOCKET NUMBER: 5524-161-999
RENCE/DOCKET NUMBER: 5624-161-999
RENCE (212)790-9090
FRAX: (212)790-9090
FRAX: (212) 869-9741
TON FOR SEQ ID No: 4:

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                     ATGTGGACCCTGGTGGCTGGCTTAACAGCAGGGCTGGTGGCTGGAACGCGGTGC
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FENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
FENTION: MODULATING PROTEINS
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PatentIn Release #1.0, Version #1.25
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Indels:
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Matches:
                                                                                                                                                                                                                                                                        3: Bristol-Myers Squibb Company 3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: ON0071A-PC TELECOMMUNICATION INFORMATION: TELEPHONE: (206)728-4800
                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02321
FILING DATE: 19910403
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                                                                                                                          401 GluHisCysCysProGln 406
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Poor, Brian W. REGISTRATION NUMBER: 32,928
                                                                                                                                                                                                      Shoyab, Mohammed
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ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
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APPLICANT: Plowman, Gre
TITLE OF INVENTION: EDI
TITLE OF INVENTION: MOD
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STATE: Washington
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GENERAL INFORMATION:
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                                        CGGGGCTTCCACTGCAGTGCAGACGGGCGATCCTGCTTCCAAAGATCAGGTAACAACTCC
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APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPTTHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
NUMBER OF SEQUENCES: 12
Sequence 2, Application US/07668648;
Patent No. 5416192;
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowan, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
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Patentin Release #1.0, Version #1.25
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-161-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
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APPLICATION NUMBER: US/07/668,648
FILING DATE: 19910819
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Patent No. 5416192
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32.00
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100.00%
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TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                            STREET: 1155 AVE
CITY: New York
STATE: New York
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REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 56
FELECOMMUNICATION INFORMATION:
                                       FILING DATE: 13-WAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,8
                                                                                                                                                TELEPHONE: (212)790-9090
TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
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100.008
4.618
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                                                                                                                                                                                                                         LENGTH: 589 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-429-998-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: EP
TITLE OF INVENTION: MO
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOVEL CYSTEINE-RICH GROWTH
                                                                                    COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/668,648
FILING DATE: 19910019
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Mismatches:
Indels:
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GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
APPLICANT: Plowman, Gregory D.
TOTAL OF INVENTION: EPITHELINS: NOVEL CYSTY
APPLICANT: MODULATING PROTEINS
STREET: 1155 Avenue of the Americas
CITY: New York
CTATE: New York
COUNTRY: USA
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1155 Avenue of the Americas
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APPLICATION NUMBER: US/08/429,998
FILING DATE: 27-APR-1995
CTACCIFICATION: 514
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                     NAME: MASTOCK, S. LOSILIO
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624
TELECOMMUNICATION INFORMATION:
TELEPAS: (212)799-9090
TELEPAS: (212) 869-9741
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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32.00
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                                                                                                                                                                                                                                                                                                                                                                                                                       : 589 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-07-668-648-6
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie &
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COMPUTER READABLE FORM:
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: New York
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Best Local Similarity:
Query Match:
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Sequence 6, Application US/08429998
Patent No. 5885961
GENERAL INFORMATION:
GAPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUFTWARE: PC-DOS/MS-DOS
SUFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,998
FILING DATE: 27-APR-1995
CLASSIFICATION: 514
PRIOR APPLICATION: 514
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                          Matches
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REFERENCE/DOCKET NUMBER: 5624-161-999 TELECOMMUNICATION INFORMATION:
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1155 Avenue of the Americas
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APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
ATTORNEY/AGENT INFORMATION:
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Gregory D. EPITHELINS: NOVEL CYSTEINE-RICH GROWTH MODULATING PROTEINS
                                                                                                   1396 GOGAGCTGGCCTGCTGCCAGTTGCCCCATGCTGTGTGCTGCGAGGA1
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                                                                                                                                                                     1456 TGCCCGGCTGCTACACCTGCAACGTGAAGGCTCGA 1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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Matches:
Conservative:
Mismatches:
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                                                                 US-09-824-647-16 (1-2095) x US-08-431-333-2 (1-589)
 Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEPROVE: (212)790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/431,333
FILING DATE: 27-APR-1995
CLASSIFICATION: 536
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APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                            Sequence 6, Application US/08431333; Patent No. 5965723; Patent No. 5965723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.12e-20
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100.00%
100.00%
4.61%
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MEDIUM TYPE: Floppy disk
Best Local Similarity: 100.00%
Query Match: 4.61%
DB: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                 APPLICANT: Shoyab, P
APPLICANT: Plowman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
APPLICANT: PLOWMAN: GREGORY D.
TITLE OF INVENTION: EPITHELINS: NOVEL CXSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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Matches:
Conservative:
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Matches:
Conservative:
Mismatches:
Indels:
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REGISTRATION NUBBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-161-999
TELECOMMUNICATION INFORMATION:
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1155 Avenue of the Americas
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FILING DATE: 27-APR-1995
CLASSIFICATION: 536
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APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08431333 Patent No. 5965723
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32.00
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TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: 2
        TYPE: amino acids
TYPE: amino acids
Olivorory: 14-
                                                                                                                                                       1.12e-20
32.00
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MEDIUM TYPE: Floppy disk
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100.00%
4.61%
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                 SEQUENCE CHARACTERISTICS
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STATE: New York
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                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
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                                                                                   , MOLECULE TYPE:
US-08-429-998-6
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                                                                                                                                          Alignment Scores
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1396 GGGAGCTGGCGCTGCTGCCAGTTGCCCCATGCTGTGTGCGGAGGATCGCCAGCACTGC 1455
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VENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
VENTION: MODULATING PROTEINS
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02321
                                                                                                                                                                                                                                                                                                US-09-824-647-16 (1-2095) x PCT-US91-02321-2 (1-589)
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Mismatches:
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Matches:
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Matches:
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3005 First Avenue
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NAME: Poor, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: 0N0071A-PC
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application PC/TUS9102321
GENERAL INFORMATION:
APPLICAMT: Shoyab, Mohammed
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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100.00%
4.61%
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                                               : 589 amino acids
AMINO ACID
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AMINO ACID
             INFORMATION FOR SEQ ID NO:
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                                SEQUENCE CHARACTERISTICS
                                                                                                ; MOLECULE TYPE: protein
PCT-US91-02321-2
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TITLE OF INVENTION: I
TITLE OF INVENTION: I
NUMBER OF SEQUENCES:
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STATE: Washington
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Best Local Similarity:
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Best Local Similarity:
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                                                                                   TOPOLOGY:
                                                                                                                                                           Alignment Scores:
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                                                 LENGTH:
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                                                                    TYPE:
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OB:
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APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 RDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REPERENCE: 29996.488/P001.A
CURRENT APPLICATION NUMBER: US/08/991,862
CURRENT FILING DATE: 1998-08-17
EARLIER APPLICATION NUMBER: 08/863,862
EARLIER PILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver: 2.0
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APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: RETHELLINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company
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480 CysProAlaGlyTyrThrCysAsnValLysAlaArg 491
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Conservative:
Mismatches:
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ATTORNET/AGENT INFORMATION:
NAME: POOL, BIIAN W.
REGISTRATION NUMBER: 32,928
RREFERNEL/DOCKET NUMBER: 0N0071A-PC
TELECOMMUNICATION:
TELEPHONE: (206)728-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US91/02321
FILING DATE: 19910403
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BEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Mouse epithelin/granulin
US-08-991-862-2
                                                                                            Sequence 2, Application US/08991862
Patent No. 6309826
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STATE: Washington
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Best Local Similarity:
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RESULT 13

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TOPOLOGY: linea
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FILING DATE: 19
CLASSIFICATION:
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                                        1396 GGGAGCTGGCCTGCTGCCAGTTGCCCCATGCTGTGCTGCGAGGATCGCCAGCACTGC 1455
                                                               1048 GAGAAGGCCCCAGCTCACCTCAGCCTGCCAGACCCACAAGCCTTGAAGAGAGATGTC 1104
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APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORICENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996.488/P001-A
FULR REPERENCE: 29996.488/P001-A
CURRENT APPLICATION NUMBER: 08/08/3,862
EARLIER APPLICATION NUMBER: 08/08/3,862
EARLIER FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (1)..(19) OTHER INFORMATION: Internal peptide of human GP88 used to develop OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPITHELINS: NOVEL CYSTEINE-RICH GROWTH MODULATING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                   1456 TGCCCGGCTGCTACACCTGCAACGTGAAGGCTCGA 1491
                                                                                                                                       Conservative:
Mismatches:
             US-09-824-647-16 (1-2095) x PCT-US91-02321-6 (1-589)
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
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Patent No. 5416192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
                                                                                                                                                                                                                         Sequence 6, Application US/08991862
Patent No. 6309826
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
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ORGANISM: Human granulin
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Best Local Similarity:
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892 TATACCTGCTGCCGTCTACAGTCGGGGGCCTGGGGCCTGCTGCTGTTT 939
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... Plowman, Gregory D.
INVERNION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
INVERTION: MODULATING PROTEINS
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SUGTREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/429,998
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
                                             ATTORNEY ACENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-161-999
REFERENCE/DOCKET NUMBER: 5624-161-999
TELEPHONE; (212)790-9090
TELEPHONE; (212)790-9090
TELEPHONE; (212) 869-9741
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-161-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 27-APR-1995
CLASSIFICATION: 514
APPLICATION NUMBER: US/07/668,648
FILING DATE: 19910819
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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AMINO ACID
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York STATE: New York
                                                                                                                                                                                                                                                                              linear
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66 TyrThrCysCysArgLeuGlnSerGlyAlaTrpGlyCysCysProPhe 81
                                                                                                                                                                                                                              CITY: Sea
STATE: Wa
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -08-991-862-7
                                                                                                                                                                                                             892 TATACCTGCTGCCGTCTACAGTCGGGGGCCTGGGGCTGCTGCCCTTTT 939
                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                              Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-824-647-16 (1-2095) x US-08-431-333-8 (1-179)
                                                                                                                                                                              US-09-824-647-16 (1-2095) x US-08-429-998-8 (1-179)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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Matches:
                                                                                                                                  Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels:
                                                                                                                                                                                                                                                                                                                                                      Shoyab, Monaumer Shoyab, Honaumer Shoyab, Gregory D. INVENTION: EPITHELINS: NOVEL CY TAVENTION: MODULATING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALPICATION NUMBER: US 07/668,648 FILING DATE: 13-MAR-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/431,333
FILING DATE: 27-APR-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/08431333 Patent No. 5965723 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misrock, S. Leslie
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2.31%
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (212) 869-9741 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
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                                                                                                                Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New York
; MOLECULE TYPE:
US-08-429-998-8
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                                                                                               Percent Similarity:
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                                                 Alignment Scores:
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                                                                                                                                 Query Match:
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APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA THORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996.488/P001-A
CURRENT APPLICATION NUMBER: US/08/991,862
                                                                   Gregory D. EPITHELINS: NOVEL CYSTEINE-RICH GROWTH MODULATING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 TyrThrCysCysArgLeuGlnSerGlyAlaTrpGlyCysCysProPhe 81
                                                                                                                                                                                                                                                                                                                                                                                                 PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-824-647-16 (1-2095) x PCT-US91-02321-8 (1-179)
                                                                                                                                                                          ADDRESSEE: Bristol-Myers Squibb Company
STREET: 3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels:
                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02321
FILING DATE: 19910403
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Sequence 8, Application PC/TUS9102321
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/08991862 Patent No. 6309826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Poor, Brian W.
REGISTRATION NUMBER: 32,928
                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EARLIER FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT FILING DATE: 1998-08-17
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100.00%
2.31%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 179 amino aci
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein PCT-US91-02321-8
                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO
                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                               Washington
                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                         Seattle
                                                                                                                                                                                                                                                                      USA
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APPLICANT: SCOTT, RANDY W.
APPLICANT: GLEICH, GERALD J.
APPLICANT: WILDE, CRAIG G.
TITLE OF INVENTION: BASOPHIL GRANULE PROTEINS
MUBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    865 GACATGGAGGTGAGCTGCCCAGATGGCTATACC 897
                                                                              865 GACATGGAGGTGAGCTGCCCAGATGGCTATACC 897
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** APPLICANT: SCOTT, RANDY W.; GLEICH, GERALD J.;
**WILDE, CRAIG G.

** TITLE OF INVENTION: BASOPHIL GRANULE PROTEINS
** NUMBER OF SEQUENCES: 8
                                                                                                      5 ASPMETGIUVALSERCYSPROASPGIYTYRTH 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS-09-824-647-16 (1-2095) x US-08-573-675-2 (1-15)
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                                    US-09-824-647-16 (1-2095) x US-08-245-853-2 (1-15)
                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Fish & Richardson
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 06514/013002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 322-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: ASCIII.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/573,675
FILING DATE: 18-DEC-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,813
FILING DATE: 11-SEP-1992
ATTOMEY/AGENT INFORMATION:
NAME: GREGG, VALETA
REGISTRATION NUMBER: 35.127
                                                                                                                                                                                                     Sequence 2, Application US/08573675 Patent No. 5747283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 854-0875
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 15 amino acids
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Best Local Similari
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3470825-2
                                       ; NAME/KEY: PEPTIDE
; LOCATION: (1)..(14)
; OTHER INFORMATION: Internal peptide of human GP88 used to develop
; OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody
US-08-991-862-7
                                                                                                                                                                                                                                                                                                                                                                          1708 GCACGCAGGGTACCAAGTGTTTGCGCAGGGAGGCCCCGCGC 1749
                                                                                                                                                                                                                                                                                                                                                                                                1 AlaArgArgGlyThrLysCysLeuArgArgGluAlaProArg 14
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                                                                                                                                                                                                                           Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SCOTT, RANDY W.
APPLICANT: GLEICH, GERALD J.
APPLICANT: WILDE, CRAIG G.
TITLE OF INVENTION: BASOPHIL GRANULE PROTEINS
TUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative:
Mismatches:
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                                                                                                                                                                                    Length:
Matches:
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REFERENCE/COCKET NUMBER: 24842-20059.20
FELLECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
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PRIOR APPLICATION DATA:
APPLICATION WUBER: US 07/943,813
FILING DATE: 11-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: BOZICEVIC, KARL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/245,853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3: MORRISON & FOERSTER
755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08245853
Patent No. 5476839
GENERAL INFORMATION:
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14.00
100.00%
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ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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ORGANISM: Human granulin
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STATE: California
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                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
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Best Local Similarity
Query Match:
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Conservative: Mismatches:

Indels:

Length: Matches:

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/106,507
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                                                                                                                                                                 Conservative
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Indels:
                                                                                                                                                                                 Mismatches:
Indels:
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Matches:
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Matches:
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                                                                                                                                                                                                                                                                                                1734 CAGGGAGGCCCCGCGCTGGGACGC 1757
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,648
FILING DATE: 08-SEP-1992
ATTORNEY/AGENT: INFORMATION:
NAME: WIGHT, CHRISTOPHER L.
                                                                                                                                                                                                                                                                                                                   32 GlnGlyGlyProAlaLeuGlyArg 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: CD27 LIGAND NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                           og US/08106507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARMITAGE, RICHARD J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GOODWIN, RAYMOND G.
GIRI, JUDITH G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: WIGHT, CHRISTOPHER L
REGISTRATION NUMBER: 31,68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
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100.00%
1.15%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KMANN, M. P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-106-507-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                     TYPE: PRT
ORGANISM: Homo sapiens
US-08-584-031-11
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                                                                                                                                                             Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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                                                                                                             Alignment Scores
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SEQ ID NO 11
                                                                                                                                                                                                        Query Match:
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DB:
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GENERAL
                                                                                                                                No.
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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APPLICANT: Bulbiteser-Brosch, Roland
APPLICANT: Bulbiteser-Brosch, Roland
APPLICANT: Billault, Alain
TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INVENTION: TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF WICE
FILE REPERRORE: 3495-0169
CURRENT APPLICATION WUMBER: US/09/060,756
CURRENT FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 743
SOFTWARE: PALENTIN Ver. 2.0
SEQ ID NO 732
                                                                                                                                                                                                        Length:
Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                          865 GACATGGAGGTGAGCTGCCCAGATGGCTATACC 897
                                                                                                                                                                                                                                                                                                                                                                                             5 AspMetGluValSerCysProAspGlyTyrThr 15
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Indels:
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                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                     US-09-824-647-16 (1-2095) x 5470825-2 (1-15)
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                 APPLICATION NUMBER: US/08/259,564
FILING DATE: 15-JUN-1994
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Patent No. 6030945
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TITLE OF INVENTION: APO-2 LIGAND
FILE REFERENCE: 11669.22US03
                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 551,263
FILING DATE: 10-JUL-1990
;SEQ ID NO:2:
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100.00%
1.59%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Ver. 2.0
 CURRENT APPLICATION DATA:
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Best Local Similarity:
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Best Local Similarity:
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                                                                                                                                LENGTH: 15
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TYPE: PRT
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CORRESPONDENCE ADDRESS:
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Patent No. 5716805
GENERAL INFORMATION:
APPLICANT: Spriggs, Melanie
APPLICANT: Stinivasan, Subhashini
TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUNG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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Conservative:
Mismatches:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,648
ILING DATE: 08 SEP-199.2
ATTORNEY/AGENT INFORMATION:
NAME: WIGHT, CHRISTOPHER I.
RESISTRATION NUMBER: 31,680
REFERENCE/DOCKET NUMBER: 2809-A
TELECHONE: 206-587-0430
INFORMATION FOR SEQ ID NO: 10:
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                                            76 GlnGlyGlyProAlaLeuGlyArg 83
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APPLICATION NUMBER: US/08/106,507
                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: BECKNANN, M. P.
APPLICANT: GOODHIN, RAYMOND G.
APPLICANT: GITI, JUDITH G.
APPLICANT: ARMITAGE, RICHARD J.
TITLE OF INVENTION: CD27 LIGAND
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                          SEE: IMMUNEX CORPORATION: 51 UNIVERSITY STREET SEATTLE
                                                                                                                                          Sequence 10, Application US/08106507
Patent No. 5573924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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Best Local Similarity:
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                                                                                                  RESULT 27
US-08-106-507-10
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SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                        OPERATING SYSTEM: Apple Operating System 7.1 SOFTWARE: Microsoft Word for Apple, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/446,922
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Mismatches:
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                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/107,353
FILING DATE: 08-13-93
CLASSIFICATION: 435
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ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
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COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION TELEPHONE: (206)587-0430
                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple O
                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia
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100.00%
1.15%
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                           COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
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Best Local Similarity:
Query Match:
                           CITY: SC.
STATE: WA
COUNTRY: USA
101
                                                                        USA
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Conservative:

Mismatches: Indels:

Gaps:

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US-09-824-647-16 (1-2095) x US-09-022-940-3 (1-230)
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                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: HUMAN LYSOPHOSPHOLIPASE
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEO for Windows Version 2.0 URRENT APPLICATION DATA:
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                                                                                                                                                                                                                          142 LeuSerCysTrpLeuProLeuArg 149
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Patent No. 5965423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMFUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
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REGISTRATION NUMBER: 36
REFERENCE/DOCKET NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 3174 Porter Dr
Palo Alto
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INFORMATION FOR SEQ ID NO
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Best Local Similarity:
                                                         Percent Similarity:
Best Local Similarity:
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Alignment Scores:
Pred. No.:
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CITY: Pa
STATE: C
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APPLICANT: Shah, Purvi
APPLICANT: Murry, Lynn E.
APPLICANT: NOVEL HUMAN LYSOPHOSPHOLIPASE
NUMBER OF SEQUENCES: 3
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Mismatches:
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSER: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                 Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1734 CAGGGAGGCCCCGCGCTGGGACGC 1757
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/844,120
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
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Patent No. 5858756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELECOMMUNICATION INFORMATION TELEPHONE: 415-855-0555
                                                                          REFERENCE/DOCKET NUMBER:
FELECOMMUNICATION INFORMAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 230 amino acids amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                       REGISTRATION NUMBER
                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                        Sest Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                   ercent Similarity
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Conservative:

Mismatches: Indels:

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Conservative:
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                                          SOFTWARE: FASTEM: DOS
SOFTWARE: FASTED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/216,001
FILLING DATE:
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APPLICANT: Shah, Purvi
APPLICANT: Wurry, Lynn E.
APPLICANT: MUTRY, LYNN E.
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS
STUTWARE: PESALSEO for Windows Version 2.0
SUGRENT APPLICATION DAYA:
APPLICATION NUMBER: US/09/216,386
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indels:
                                                                                                                                                                                                                                                       NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0329 US
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                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/878,862
FILING DATE:
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                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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LENGTH: 230 amino aci
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte PA
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1552244
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Query Match:
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIBRARY:
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**APPLICANT: #111man, Jennifer L.

**APPLICANT: Shah, Purvi
**APPLICANT: Shah, Purvi
**TITLE OF INVENTION: HUMAN LYSOPHOSPHOLIDASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTE: CA
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APPLICANT: Corley, Neil C.
APPLICANT: MULTY, Lynn E.
TITLE OF INVENTION: NEW HUMAN LYSOPHOSPHOLIPASE
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,940
FILING DATE: Filed Herewith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Billings, Lucy J.
REGISTRATION UDMBER: 36,74
REFERENCE,POCKET NUMBER: PELECOMMUNICATION INFORMATION
TELEPHONE: 650-855-0555
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                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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100.00%
1.15%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
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US-09-022-940-5 .
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Best Local Similarity:
Query Match:
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Pred. No.:
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STATE: CITY:

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STREET:
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Pred. No.:
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                             Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: HUMAN LYSOPHOSPHOLIPASE
NOMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                    1686 CTGTCCTGCTGCTTCCGCTGCGC 1709
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APPLICATION NUMBER: US/09/216,386
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APPLICATION NUMBER: 09/022,940
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No. 6093561
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REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-TELECOMMUNICATION:
TELEPHONE: 650-855-0555
                                                           ELECOMMUNICATION INFORMATION TELEPHONE: 650-855-0555
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                                                                                             TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 230 amino acid
TYPE: amino acid
                                                                                                                                                                                        single
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                      TOPOLOGY:
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APPLICANT: Shah, Purvi
APPLICANT: Corley, Nell C.
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: NEW HUMAN LYSOPHOSIPASE
NUMBER OF SEQUENCES: 4
                                 Conservative:
Mismatches:
Indels:
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Mismatches:
Indels:
Gaps:
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                                                                                                                     US-09-824-647-16 (1-2095) x US-09-216-386-5 (1-230)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYSTEM: DOS
FastSEQ for Windows Version 2.0
Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                Incyte Pharmaceuticals, Inc
                                                                                      Gaps:
                                                                                                                                                        1686 CIGICCIGCIGCTICCGCIGCGC 1709
                                                                                                                                                                       142 LeuSerCysTrpLeuProLeuArg 149
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APPLICATION NUMBER: US/08/878,862
FILING DATE: Herewith
                                                                                                                                                                                                                                                              Sequence 3, Application US/08878862 Patent No. 6143544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3: Diskette
IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 230 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATELEPHONE: 415-855-055: TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Billings, Lucy J
REGISTRATION NUMBER: 3
REFERENCE/DOCKET NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM MEDIUM TYPE: Disket
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
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CA
                                 Percent Similarity:
Best Local Similarity:
Query Match:
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Query Match:
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1686 CIGICCIGCIGGCIICCGCIGCGC 1709

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Alignment Scores

Conservative: Mismatches: Indels:

Gaps:

Matches: Length:

ADDRESSEE:

COUNTRY:

COMPUTER:

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APPLICANT: Baldwin, Donald A.
APPLICANT: Briggs, Steven P.
APPLICANT: Crane, Virginia C.
TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses FILE REFERENCE: 5718-44,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-372-422A-26
US-09-372-422A-26
Sequence 26, Application US/09372422A
Patent No. 6313375
GENERAL INFORMATION:
APPLICANT: Rudolf Jung
TITLE OF INVENTION: Malze Aquaporins and Uses Thereof
FILE REFERENCE: 0919
CURRENT APPLICATION: Malze
CURRENT APLICATION: 1999-08-11
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NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 26
LENGTH: 272
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CURRENT FILING DATE: 1999-03-31
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PRIOR APPLICATION NUMBER: US 60/098,692
PRIOR FILING DATE: 1998-08-31
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Patent No. 6287843
GENERAL INFORMATION:
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8.00
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Best Local Similarity:
Query Match:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Zea mays US-09-372-422A-26
                                                                                                                                                                   ; ORGANISM: Zea mays
US-09-372-422A-28
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                                                                                                                                                   TYPE: PRT
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DB:
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No.:
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APPLICANT: Francois Barrieu
FITLE OF INVENTION: Maize Aquaporins and Uses Thereof
FILE REFERENCE: 0919
                                                                                                                                                                 APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: NOVEL HUMAN LYSOPHOSPHOLIPASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                   Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT, APPLICATION NUMBER: US/09/372,422A
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               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/844,120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/213,394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 28, Application US/09372422A Patent No. 6313375
GENERAL INFORMATION:
                                                                                                          Sequence 3, Application US/09213394
Patent No. 6319701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749 REFERENCE/DOCKET NUMBER: PF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                 STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM Compatible
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8.00
100.00%
100.00%
1.15%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                                                                              94304
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Pred. No.:
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Conservative: Mismatches: Indels:

Length: Matches:

US-09-213-394-3

Query Match:

core:

RESULT 38

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SODIUM-DEPENDENT
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                                                                                                                                                                                                                                              Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Lal, Preet,
APPLICANT: Bandman, Olga
TITLE OF INVENTION: NOVEL HUMAN SODIUM-DEPENI
TITLE OF INVENTION: PHOSPHATE CO-TRANSPORTER
                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                               Matches:
                                                                                                                                                                                                                                                                                          Indels:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,118
FILING DATE: Filed Herewith
CLASSIFICATION 1435
PRIOR APPLICATION TOWNER:
APPLICATION NUMBER:
APPLICATION WOMBER:
APPLICATION WOMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0221 US
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                          1231 GCTGGGGCAGCAGTGCTGGTGGT 1208
                                                                                                                                                                                                                                                                                                                                                                                                         66 AlaGlyGlySerSerAlaGlyGly 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08805118 Patent No. 5985604
  CURRENT FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 743
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 727
LENGTH: 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 401 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                      ; TYPE: PRT
; ORGANISM: Mycobacterium sp.
US-09-060-756-727
                                                                                                                                                                                                                                                                                          .168
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Pred. No.:
Score:
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                                                                                                                                                                                                             Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA FILE REFERENCE: 3495-0169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Baldwin, Donald A.
APPLICANT: Briggs, Steven P.
APPLICANT: Crane, Virginia C.
TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                     Mismatches:
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CURRENT APPLICATION NUMBER: US/09/282,305
CURRENT FILING DATE: 1999-03-31
PRIOR PILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
LENGTH: 305
                                                                                                                                                                                                                                                                                          Indels:
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APPLICANT: Buchrieser Brosch, Roland
APPLICANT: Gordon, Stephen
APPLICANT: Billault, Alain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/09282305
Patent No. 6287843
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 18
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Best Local Similarity:
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Query Match:
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                                                                                                    ; TYPE: PRT
; ORGANISM: Zea mays
US-09-282-305-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                            SEQ ID NO 14
LENGTH: 302
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DB:
                                              SOFTWARE:
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RESULT 45

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TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
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                                                                                                                                                                                                                                                                                                                         ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-824-647-16 (1-2095) x US-08-724-394A-11 (1-480)
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/724,394A FILING DATE: 01-02-1996 CLASSIFICATION: 536 ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                380 CCATCCAGTGCCCTGATAGTCAGT 403
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Job time: 57 secs
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LOCATION: 1..480
OTHER INFORMATION: /note= "NPT4"
Application US/08724394A
                                                                                   APPLICANT: Kronmal, Gregory S. APPLICANT: Lauer, Peter M. APPLICANT: Ruddy, David A. APPLICANT: Thomas, Winston APPLICANT: Tsuchihashi, Zenta APPLICANT: Wolff, Roger K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.00%
100.00%
1.15%
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                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA;
ZIP: 94111-3834
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
              Patent No. 5872237
GENERAL INFORMATION:
APPLICANT: Feder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity:
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Porphyromonas ging Mouse GP88 autocri Human API-108 tryp Human peptide #107 PDGF inhibitor (PG

Human TSH receptor Chlamydial VDI epi Oestrogen receptor Peptide sensor TUK LXXLL signature mo Vascular endotheli Melanoma-specific Melan A/MART epito Human cancer antig Human cancer antig Human cancer antig

E.Coli 50s ribosom

Coactivator leucin

Human GP88 autocri BGP N-terminal fra Basophil granule p N-terminal amino a

N-terminal amino a

Description

Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Word size:

Searched:

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Transforming frowth factor e; cell proliferation; mitogen
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SUMMARIES
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ABB52180
AAM97797
AAR67120
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AAY06031
AAY06039
AAX06025
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AAW82826
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                                                       Query
Match Length
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694
1 cgcaggcagaccatgtggac.....ataaagtttgtcactttctt 2095
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/SIDSZ/goddatu/geneseq/geneseqp-embl/AA1991 DAT:*
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            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

    protein search, using frame_plus_n2p model

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seqs, 133250620 residues
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Maximum DB seq length: 15
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Synthetic peptide Synthetic peptide HLA binding TADG-1 HLA binding TADG-1 HLA binding TADG-1 HLMAN NY-ESO-1 HLA Immunogenic peptid

New bradykinin ana TSK protein tyrosi Chlamydial MOMP VD

Cytomodulating lip Human cancer antig

Jatabase

Human cancer antig

cancer antig Peptide sensor TUK Bifidobacterium bi

trachomatis MOM

92WO-US08417

02-OCT-1992;

Homo sapiens

W09307173-A. 15-APR-1993

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS2/gcgdata/geneseg/genesegp-embl/AA2001.DAT:* /SIDS2/gcgdata/geneseg/genesegp-embl/AA2002.DAT:*

D-form Interleukin

Cancer testis tumo

Peptide sensor TUK HLA Class I motif

comprising amino (75). GP88 is an 88

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8; Page 45; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scott RW, Gleich GJ,
                                                                                                                                                GP88-expressing cells
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                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                   14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-JUL-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                 19-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9201000-A.
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                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                     Sequence
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  Example
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                                                                                                                                                                                                                Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Composition containing antagonist of growth factor GP88 - useful for treating cancer and viral diseases and also for diagnosing disease from altered GP88 expression
                                                                                                                                                          TGFe is a glycoprotein with an Mr of about 25,000. The partial amino acid sequence of purified bovine TGFe indicated no homology to other known growth factors. However the N-terminal sequence exhibits considerable amino acid sequence identity to the deduced N-terminal amino acid sequence of human granulin A and the N-terminus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ranulin; epithilin; human; growth factor; autocrine; tumour; viral infection; antagonist; therapy; diagnosis; antigen;
                                                                                              Transforming growth factor E produced in commercial quantities used for wound healing and burns treatment, comprises monomeric protein which acts as mitogen for fibroblasts
                                                                                                                                                                                                                                                                                                                                                             853 GATGTGAAATGTGACATGGAGGTGAGCTGCCCAGATGGCTATACC 897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human GP88 autocrine growth factor antigenic peptide A14R.
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Matches:
Conservative:
Mismatches:
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                                   (UYGE-) UNIV GEORGIA RES FOUND INC.
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                                                        Parnell PG;
                                                                                                                                         Example; Page 49; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                          AAW85481 standard; Peptide; 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     970S-0991862.
970S-0863079.
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                91US-0770585.
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                                                         Mcgraw RA,
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                                                                             WPI; 1993-134386/16.
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Best Local Similarity:
                                                                                                                                                                                                                                      Sequence 15 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            granulin;
                                                                                                                                                                                                                   of epithelin 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-DEC-1997;
23-MAY-1997;
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                 03-OCT-1991;
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                                                          Halper J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer;
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DB:
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A patient with a form of chronic myelogenous leukemia underwent two treatments of cytophoresis from which basophils were recovered. These were used to search for novel basophil granule proteins (BGP). The proteins were fractioned. Ca. 25 peaks were identified. Several fractions were pure enough to allow for the determination of a single amino acid sequence. The N-terminal sequences of eight
                                                                                                                                                                                                                               Antagonists to
This is the amino acid sequence of peptide A14R, comprising amino acid residues A566-R579 of human GPB8 (see AAM56475). GPB8 is an 8 kpa ajvoprotein autocrine growth factor that is expressed in a tightly regulated manner in normal cells, is overexpressed and unregulated in highly tumorigenic cells derived from normal cells, and which acts as a stringently required growth stimulator for the tumorigenic cells. Al4R was used in an attempt to raise neutralising antibodies to GPB8 (see also AAW5480). Antagonists GPB8, such as anti-GPBB antibodies, are used to treat diseases associated with increased expression of GPB8, particularly cancer but also viral infections. Anti-GPB8 antibodies can also be used
                                                                                                                                                                                                                                                                                                                                    but also viral infections. Anti-GP88 antibodies can also be used as diagnostic reagents and to deliver toxins or other compounds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New basophil granule proteins obtd. from cytoplasmic granules for diagnosis and treatment of pathologies involving inflammatory and IgE-mediated responses, infection, hypersensitivity and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1708 GCACGCAGGGGTACCAAGTGTTTGCGCAGGGGGCCCCGCGC 1749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Basophil granule protein; chronic myelogenous leukemia.
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Matches:
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Transforming growth factor E produced in commercial quantities - used for wound healing and burns treatment, comprises monomeric protein which acts as mitogen for fibroblasts
                                                                                                                                                                                                                                                                                         Transforming frowth factor e; cell proliferation; mitogen.
                                GACATGGAGGTGAGCTGCCCAGATGGCTATACC 897
                                               5 AspMetGluValSerCysProAspGlyTyrThr 15
                                                                                                                                                                                                                                                   N-terminal âmino acid sequence of epithelin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYGE-) UNIV GEORGIA RES FOUND INC.
                                                                                                                                       AAR35078 standard; protein; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             910S-0770585.
                                                                                                                                                                                                         09-AUG-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Halper J, Mcgraw RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1993-134386/16:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                              WO9307173-A.
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                              865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR51665 shows an N-terminal sequence of a basophil granule protein. The BGP can be extracted from human basophil granules by treatment at pH 9.0 or greater. This can be used to generate its corresponding nucleic acid an antibodies. Anti-BGPs are useful for the diagnosis of prepathologic conditions as well as chronic and acute diseases, such as parasitic infection and leukaemia, where there is a change in the amount or distribution of BGPs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human basophil granule proteins - and related nucleic acid, expression systems, antibodies, etc., for diagnosis and treatment of e.g. inflammation, parasitic infection, leukaemia etc.
such fractions are represented in AAR20736-42 and AAR22455.
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                                                                                                                                                                                                                                                            865 GACATGGAGGTGAGCTGCCCAGATGGCTATACC 897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ophil granule protein; N-terminal sequence; specific antibodies; Antibodies; Leukaemia
                                                                                                                                                                                                                                                                               AspMetGluValSerCysProAspGlyTyrThr 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Basophil granule protein N-terminal sequence
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                        AAR51665 standard; protein; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gleich GJ, Scott RW, Wilde CG;
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                                                                                           0.296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                24-OCT-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (INCY-) INCYTE PHARM INC. (MAYO-) MAYO FOUNDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.296
11.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1994-118398/14
                                                                                                                                                     Best Local Similarity:
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Best Local Similarity:
Query Match:
                                          15 AA
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                                                                                                                                Percent Similarity:
                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9406829-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAR-1994
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                                          Seguence
                                                                                                                                                                                                                                                                                                                                                                                                              AAR51665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Basoph11
                                                                                                                                                                    Query Match:
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02
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                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pared.
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Parnell PG;

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Porphyromonas gingivalis; protective epitope; antiinflammatory; vaccine;
                                  TGFe is a glycoprotein with an Mr of about 25,000. The partial amino acid sequence of purified bovine TGFe indicated no homology to other known growth factors. However the N-terminal sequence exhibits considerable amino acid sequence identity to the deduced N-terminal amino acid sequence of human granulin A and the N-terminus
                                                                                                                                                                                                                                              40000
                                                                                                                                                                                                                                                               Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Porphyromonas gingivalis PrtR27 peptide #6.
                                                                                                                                                                                                                                            Length:
                                                                                                                                                                                                                                                                                                                             Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-824-647-16 (1-2095) x AAR35078 (1-14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB14948 standard; peptide; 13 AA.
Example; Page 49; 60pp; English.
                                                                                                                                                                                                                                          24.3
9.00
100.00%
100.00%
1.30%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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97US-0991862. 97US-0863079.

16-DEC-1997; 23-MAY-1997;

(SERR/) SERRERO G.

98WO-US10555

22-MAY-1998; 26-NOV-1998

WO9852607-A1.

Mus sp.

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The present sequence is one of twenty overlapping peptides corresponding to the N-terminal 148 residues of the PrER27 adhesin from Porphyromonas of the N-terminal 148 residues of the PrER27 adhesin from Porphyromonas gingivalis. Antibodies directed towards the PrEZ7 adhesin were found to provide protection against periodontitis in a human patient and immunoprotected mice. The peptides comprising at least one P. gingivalis epitope periodontesin. Peptides comprising at least one P. gingivalis epitope are useful in the treatment and prevention of periodontal disease, particularly periodontitis, which is associated with P. gingivalis infection. The peptides are useful as immunosens in vaccine formulations infection. The peptides are useful as immunosens in vaccine formulations for active immunisation. They may also be used to generate protecting and peptide-specific antiserum useful for passive immunisation, and to generate polycional or monoclonal antibodies. The immunisation and antibodies against the peptides can be used in diagnostic tests to detect P. gingivalis infection. The antibodies can also be used in oral compositions such as toothpaste and mouthwash to neutralise the
periodontal disease; periodontitis; immunogen; infection; PrtR27 adhesin.
                                                                                                                                                                                                                                                                                                                                          New compositions comprising at least one peptide with an epitope of Arg-specific proteinase associated with Lys-specific proteinase protein complex for treating and preventing periodontitis-associated Porphyromonas ginglyalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ranulin; epithilin; mouse; growth factor; autocrine; tumour; viral infection; antagonist; therapy; diagnosis; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse GP88 autocrine growth factor antigenic peptide S14R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-824-647-16 (1-2095) x AAB14948 (1-13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1029 GGGCCCTGTTCACAGGTACC 1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ė
                                                                                                                                                                                                                                           (VICT-) VICTORIAN DAIRY IND ASSOC.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 21; 62pp; English.
                                                                                                                                                                                                                                                                               O'Brien-Simpson NM, Reynolds EC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW85479 standard; Peptide; 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antigen and prevent disease
                                                                                                                                                                             99AU-0008939.
                                                                                                                                           01-MAR-2000; 2000WO-AU00142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.00%
100.00%
1.02%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2e+03
7.00
                                         Porphyromonas gingivalis
                                                                                                                                                                                                               UYME ) UNIV MELBOURNE
                                                                                                                                                                                                                                                                                                                 WPI; 2000-579275/54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GP88; granulin;
                                                                                                                                                                                                                                  CSL LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                         WO200052041-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                              01-MAR-1999;
                                                                                                           08-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer; vi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW85479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred.
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          MAKE X B X B X B X B X
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This is the amino acid sequence of peptide S14R, comprising amino acid residues S562-R575 of murine GP88 (see AAW85474). GP88 is an 88 kDa glycoprotein autocrine growth factor that is expressed in a tightly regulated manner in normal cells, is overexpressed and unregulated in highly tumorigenic cells derived from normal cells, and which acts as a stringently regulated growth stimulator for the tumorigenic cells. S14R was used to raise neutralising antibodies to GP88. Antagonists to GP88, auch as anti-GP88 antibodies, are used to treat diseases associated with increased expression of GP88, particularly cancer but also viral infections. Anti-GP88 antibodies can also be used as diagnostic reagents and to deliver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; neuroprotective; nootropic; gene therapy; vaccine;
Alzheimer's disease; Alzheimer's Disease-Associated Feature; AF;
Alzheimer's Disease-Associated Protein Isoform; API; tryptic digest;
Expression Reference Protein Isoform; ERPI; proteolysis.
                                                                                                                                                                                                                                            - useful for
                                                                                                                                                                                                                                          Composition containing antagonist of growth factor GP88 - useful for treating cancer and viral diseases and also for diagnosing disease from altered GP88 expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4,0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coxins or other compounds to GP88-expressing cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human API-108 tryptic digest peptide #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-824-647-16 (1-2095) x AAW85479 (1-14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1714 AGGGGTACCAAGTGTTTGCGC 1734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB52180 standard; Peptide; 14 AA.
                                                                                                                                                                                                                                                                                                        Example 8; Page 45; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.98e+03
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100.00%
100.00%
1.01%
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                                                                                                                                                                                                                         WPI; 1999-045276/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200175454-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                              Serrero G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB52180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB52180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score:
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The present invention relates to oligonucleotides (see AAL26793-AAL34659) encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoletin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-protein coupled receptors and thioesterases. The present sequence is a peptide encoded by one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that make prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic organisms.
                                                                                                                                                                                                                                                             Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autolmmune diseases and infections -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             platelet derived growth factor; PDGF; smooth muscle; mimic; interaction site; constrained conformation; inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PDGF inhibitor (PGF-3), contg. proline brackets.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 3902; 4143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-824-647-16 (1-2095) x AAM97797 (1-14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        264 CCCCTTCCCAGAGGCCGTGGC 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR67120 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 ProLeuProArgGlyArgGly
                                                            28-DEC-1999; 99US-0173419.
27-DEC-2000; 2000US-0173419.
                    28-DEC-2000; 2000WO-US35498.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.98e+03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JUN-1995 (first entry)
                                                                                                                                                                         Leach M;
                                                                                                                           (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                   WPI; 2001-465210/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                         Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9425482-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR67120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR67120
neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; angiopietin; gene therapy; vaccine; amylase; cancer; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinase; colony stimulating factor; interleuklin; G-protein coupled receptor; thioesterase; inflammation; nervous system disease; autoimmune disease; infection;
                                                                                                                                                                                                                                                                                                                            Screening for Alzheimer's disease in a mammal, by making two-dimensional array of a feature whose relative abundance correlates with disease, and comparing with abundance of the feature in samples of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   order to determine whether a patient is suffering from, or has a predisposition to, Alzheimer's Disease. The relative abundance of the AFs and APIs correlates with the severity of Alzheimer's Disease. The present sequence is a peptide produced from an API by proteolysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to methods for the screening, diagnosis and prognosis of Alzheimer's disease. The methods involve the detection of Alzheimer's Disease-Associated Features (AFs) and Alzheimer's Disease-Associated Protein Isoforms (AFIs) in cerebrospinal fluid,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       serum or plasma. The abundance of the AFs and APIs is then normalised to an Expression Reference Protein Isoform (ERPI) in
                                                                                                                                                                                            Kimmel LH, Parekh RB;
er TR, Sunderland PT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human peptide #1072 encoded by a SNP oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4,0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
                                                                                                                                                                                       Durham KL, Friedman DL, Herath HMAC, Kimmel
Potter DM, Rohlff C, Silber BM, Stiger TR,
Townsend RR, White F, Williams SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-824-647-16 (1-2095) x ABB52180 (1-14)
                                                                                                                           (OXFO-) OXFORD GLYCOSCIENCES UK LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1009 GGTACCTGTGAACAGGGGCCC 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM97797 standard; Peptide; 14 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GlyThrCysGluGlnGlyPro 7
                                                                                                                                                                                                                                                                                                                                                                                                                                         Example; Page 29; 162pp; English
                03-APR-2001; 2001WO-US10908.
                                                          03-APR-2000; 2000US-194504P.
28-NOV-2000; 2000US-253647P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.98e+03
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                                                                                                                                                                                                                                                                                WPI; 2001-639384/73
                                                                                                                                                (PFIZ ) PFIZER INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 AA;
                                                                                                                                                                                                                                                                                                                                                                                               healthy persons
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Alignment Scores:

Score:

Query Match:

Sequence

40200147944-A2

05-JUL-2001

Homo sapiens

24 - JAN - 2002

AAM97797;

6 RESULT

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may

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800000

Length:
Matches:
Conservative:
Mismatches:
Indels:

3.31e+07 6.00 100.00% 100.00% 0.86%

Gaps: (1-8)

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Peptides with affinity to human TSH (thyroid stimulating hormone) receptor antibody are used for detection of the antibody: (See also AAR73201-592).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           To obtain a poliovirus-1 (PV1)/Chlamydial hybrid, the PV1 Mahoney CDNA clone PT/XLD was modified to encode epitopes from C. trachomatis ser. A MOMP VDI. The VOI sequence was not restricted to the known epitope given in AAR66356, or to the sequence given in AAR66383 (expressed in previously described hybrids), but instead included adjacent sequences from VDI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New hybrid picornaviruses expressing chlamydial epitopes to develop prods. for vaccination, diagnosis, treatment of chlamydial infections and prodn. Of immunological reagents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chlamydial epitope; variable domain; MOMP; major outer membrane protein; picorna virus; vaccine; PV1; diagnostic; therapeutic; poliovirus; capsid protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 19; 99pp; English.
               Example 1; Page 11; 54pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR66383 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                             1517 CCCAGCCTGCCACCTTCC 1534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chlamydia trachomatis serovar A.
                                                                                                                                                                                                                                                                                                           US-09-824-647-16 (1-2095) x AAR73224
                                                                                                                                                                                                                                                                                                                                                                94WO-CA00262.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93US-0060978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CONN-) CONNAUGHT LAB LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caldwell HD, Klein MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chlamydial VDI epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1995-006796/01
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Best Local Similarity:
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                                                                                                                        8 AA;
                                                                                                                                                                                                                 Percent Similarity:
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                                                                                                                           Sequence
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                                                                                                                                                                                                                                                         Query Match:
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Q
                                                                                                                                                                                   Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
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                                                                                                                                                                                                        Score:
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are deriv. from PDGF peptides that contain proline or proline/cysteine brackets. These peptides that contain proline or proline/cysteine brackets. These peptides contain one or more interaction sites of interest. The dose is 5.5000 microcomoles. The peptides interact with specific receptors and inhibit the migration of macrophages, and thus inhibits the pro-inflammatory effects of the interleukin. The data collected demonstrates that interaction sites possess activity when present in a polypeptide that differs from the native form. Inclusion of conformation-constraining moleties can have desirable effects on an interaction site. (Also see AAR67011-117 and AAR67121-52 for analogues of other biologically active peptides conformation interaction site flanked
                                                                                                                                                                Peptide homologue or analogue with constrained conformation - has proline residues flanking the interaction site to impart greater, or more stable, biological activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel polypeptide(s) having affinity for the human TSH receptor antibody - used in detection of the TSH antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thyroid stimulating hormone receptor; TSH; human; Homo sapiens; antibody; affinity; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   by conformation constraining gps., eg. RGD peptides.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human TSH receptor (residues 47-54).
                                                                                                                                                                                                                                                Example 3; Page 39; 57pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR73224 standard; Peptide; 8 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                270 CCCAGAGGCCGTGGCATG 287
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       93US-0143364
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                                                                                                                                   WPI; 1994-358186/44.
                                                                                               Evans HJ, Kini RM;
                                           (EVAN/) EVANS H J. (KINI/) KINI R M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
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       29-OCT-1993;
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Query Match:
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nseq

Oomen RP

Murdin AD,

Length: Matches: Conservative: Mismatches:

3.31e+07 6.00 100.00% 100.00%

Nuclear hormone receptor; sensor peptide; receptor binding; screening;

AAY13573 standard; peptide; 8 AA

30-JUL-1999 (first entry)

AAY13573;

Peptide sensor TUK-1390.

modulator. Synthetic.

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Human; oestrogen receptor activity inhibitor; anti-oestrogen; diagnosis; preast cancer; estrogen; tumour; phosphotyposyl partide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a composition comprising an isolated oestrogen receptor activity inhibiting (anti-oestrogen) peptide. The peptides used in the composition comprise sequences of human oestrogen receptor (OR) surrounding Tyr537 and steroid receptor co-activator-1 (SCR-1). The peptide compositions, nucleic acids and vectors of the present invention can reduce OR activity in a cell, reduced OR polypeptide dimerisation in a cell and reduce the binding of SRC-1 polypeptide to an OR polypeptide dimer in a cell. They can be used for killing cancer cells and treating cancers, particularly breast cancer. The present sequence represents a specifically claimed anti-oestrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New anti-oestrogen peptide compositions - comprise sequences based on oestrogen receptor and steroid receptor co-activator-1 sequences, used for treating cancers
                                                                                                                                                                                                                                                                                                        breast cancer; estrogen; tumour; phosphotyrosyl peptide; malonyltyrosyl peptide; steroid receptor co-activator-1.
    00
                                                                                                                                                                                                                                                          Destrogen receptor activity inhibiting peptide #1.
 Indels:
Gaps:
                                      US-09-824-647-16 (1-2095) x AAR66383 (1-8)
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                                                                      AAW82944 standard; peptide; 8 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-US07711.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              970S-0043545
                                                                                                                                                                                                                             04-FEB-1999 (first entry)
0.86%
16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-594522/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 AA;
                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                   409846250-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pietras RJ;
                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                AAW82944;
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Query Match:
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                                                                                                                                    RESULT 13
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Shan B;

Lustig K,

Chen J,

Baeuerle P, Beckmann H,

WPI; 1999-347794/29.

(TULA-) TULARIK INC.

30-SEP-1998; 21-NOV-1997;

980S-0163713. 970S-0975614.

.98WO-US24969

:0-NOV-1998;

WO9927365-A1

03-JUN-1999.

Nuclear hormone receptor drug screens

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binding reaction occurs in solution. The sensor peptide obviates the need to include a natural coactivator protein of the receptor in the mixture. Sequences AAVI3571-587 represent examples of sensor peptides that can be used in the method of the invention.
                                                                            hormone receptor function. The methods use a sensor peptide covalently coupled to a detectable label, that provides direct, in vitro ligand-dependent binding to a nuclear hormone receptor. Panels of predetermined or randomized candidate sensors are readily screened for receptor binding. The methods and compositions provide for efficient screening of modulators of nuclear hormone receptor function, without the use of cell- or gel-based steps. The methods are amenable to automated, cost-effective high throughput screening of chemical libraries for
                                                                                                                                                                                                                                                                                                 bloactive compounds. To ensure specificity and optimize binding, the sensor is generally present at sub-micromolar concentration and the
                                                        The invention provides methods for screening of modulators of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        890000
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW67665 standard; peptide; 8 AA.
Claim 7; Page 17; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1131 CTCCTCCGATACCTGCTG 1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LeuLeuArgTyrLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.31e+07
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ID AAW6
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AC AAW6
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Conservative: Mismatches: Indels:

100.00% 100.00% 0.86%

Percent Similarity: Best Local Similarity:

Score:

Query Match:

US-09-824-647-16 (1-2095) x AAW82944 (1-8)

1131 CTCCTCCGATACCTGCTG 1148

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Length: Matches:

3.31e+07

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/note= "H4/D4 nicotinylated"

Location/Qualiflers

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subunit L17 identified and characterised using a novel method of the invention. The invention comprises a method for labeling a protein by protecting epsilon-amino groups of Lys, cleaving the protein by protecting epsilon-amino groups of Lys, cleaving the protein to produce a mixture of peptides and treating these with a labeling agent that binds to the N-terminal amino acid. The method is used for identifying proteins, e.g. for analysis of proteins expressed by cells in different expression states. The method makes possible relative protein esparation in one- or two-dimensional gel separations, even when separation is only partial, and facilitates de novo sequencing and automated interpretation of mass spectra. Protection of Lys sidechains ensures specific labeling of the N-termini, increases the intensity of the bings.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Method for labeling proteins, useful for identification, particularly in expression analysis, by blocking lysine sidechains, proteclysis and N-terminal labeling of peptide fragments
50S; L17; protein sequencing; protein quantitation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 2A; 27pp; English
                                                                                                                                                                                                                                                                                                                                                                       (PROT-) PROTEOME SYSTEMS LTD
                                                                                                                                                                                                                                                                                                                         03-APR-2000; 2000AU-0006643.
                                                                                                                                                                                                                                                                                 03-APR-2001; 2001WO-AU00366,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-017393/02.
                                                         Escherichia coli
                                                                                                                                                                                             WO200174842-A1
                                                                                                                                                                                                                                   11-0CT-2001.
                                                                                                       Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                            James P;
           into sequence tepteseuts on manus nucreal protein. This peptide
in the DNA binding domain (DBD) of the SRCia protein. This peptide
corresponds to amino acids 748-75 of SRCia-DBD. The invention relates
corresponds to amino acids 748-75 of SRCia-DBD. The invention relates
corresponds to amino acids 748-75 of SRCia-DBD. The invention relates
corresponds to amino acids in the inclear protein (RI) and a region on
a nuclear receptor (R2), where: (i) R1 is a signature motif; (ii) where: (i) R1 is a signature motif; (iii) the nuclear protein is a bridging factor
responsible for interaction between a liganded nuclear receptor and a
responsible for interaction between a liganded nuclear receptor and a
responsible for interaction between a liganded nuclear receptor and a
responsible for interaction between a liganded nuclear receptor during
of a nuclear protein which binds to a liganded nuclear receptor during
of a nuclear protein which binds to a liganded nuclear receptor during
to be useful in the treatment of any disease mediated through any
interaction between a signature motif on a nuclear protein and a nuclear
receptor, for example inflammation and cancer.
                                                                                                              cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence represents an LXXLL nuclear protein signature motif found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identification of inhibitors of nuclear protein/nuclear receptor interaction - useful for, e.g. treatment of disease mediated through the interaction such as inflammation and cancer
                                                                                                         Nuclear protein; signature motif; receptor protein; inflammation; interaction; inhibitor; inhibition; transcription factor; ligand.
                                                              LXXLL signature motif #5 from protein SRCla DNA binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    890000
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                         30-APR-1997;
                                                                                                                                                                                                                                                                                                                              28-APR-1998;
                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                      WO9849561-A1
                                                                                                                                                                                                                                                                                 05-NOV-1998.
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b-ions (permitting full-length sequence coverage for peptides of m/z over 1000) and allows differentiation between Lys and Glu. The use of different isotopic labels allows different proteins in the same gel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vascular endothelial growth factor receptor-2 peptide modulator #121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vascular endothelial growth factor receptor-2; VEGFR-2; VEGF modulator; psoriasis; rheumatoid arthritis; retinopathy;
                                                                                                                                       890000
                                                                                                                                                                      Conservative:
Mismatches:
Indels:
                                                                                                                                       Length:
Matches:
                                                                                                                                                                                                                     Gaps:
                                                                                                                                                                                                                                                        (1-8)
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                                                                                                                                                                                                                                                    US-09-824-647-16 (1-2095) x AAU09998
                                                                                                                                                                                                                                                                                       839 GCAGGCAGCTTAGTGAGG 822
                                                                                                                                                                                                                                                                                                                                                                                        AAU73544 standard; Peptide; 8
                                                                                                                                                                                                                                                                                                         3 AlaGlySerLeuValArg
                                                                                                                                        3.31e+07
                                                                                                                                                      6.00
100.00%
100.00%
0.87%
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                          spot to be quantified
                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                            8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-MAR-2002
                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                            AAU73544;
                                                                                              Sequence
                                                                                                                                                                                                         Query Match:
                                                                                                                                               ..
9
                                                                                                                                                                                                                                                                                                                                                           RESULT 17
                                                                                                                                                                                                                                                                                                                                                                          AAU73544
                                                                                                                                                               score:
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Gaps:

US-09-824-647-16 (1-2095) x AAW67665 (1-8)

1131 CTCCTCCGATACCTGCTG 1148

ö g

E.Coli 50S ribosomal subunit L17 peptide.

(first entry)

12-MAR-2002

AAU09998;

AAU09998 standard; peptide; 8 AA

RESULT 16 AAU09998

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modulator of VEGF function. The compound is useful for: treating a pattent suffering from poorlasts, rheumatoid arthritis, retinopathy and cancer; for imaging and assessing neovascularisation during anglogenesis; for detecting VEGFR-2 receptor or related receptor on living cells, as a calibration standard for quantitating the activities of candidate VEGFR-2 screening; as blocking reagent in random peptide screening i.e. in screening for new families of VEGFR-2 peptide ligands; in the co-crystallisation with VEGFR-2; in inhibiting or decreasing the proliferation and growth of vascular endothelial cell growth factor dependent cell lines e.g. human umbilical vein endothelial cells (HUVEC) and other research and disposite applications where VEGFR-2 is
                                                                                                                                                                                                                                                                                                                                Novel compounds having affinity for vascular endothelial growth factor receptor-2 useful for treating cancer, retinopathy, rheumatoid arthritis, psoriasis and as anglogenesis imaging agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antagonised. Agonists are useful for the treatment of diseases such as coronary artery disease. This sequence is a peptide modulator of the vascular endothelial growth factor receptor-2 (VEGF-2) based on the generic peptide sequence AAS73422, described in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                         Invention describes a compound having affinity for vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Melanoma; immunogen; epitope; homologue; vaccine; immunotherapy;
cytotoxic T cell; lymphocyte; HLA-A2.
cancer; cytostatic; ophthalmological; neovascularisation; anglogenesis; coronary artery disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Melanoma-specific mutant immunogen epitope 9mer peptide.
                                                                                                                                                                                                                                                                    Balu P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      890000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                  Mozsgai CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                     Claim 19; Page 40; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR82184 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1832 TGGGGTCCCGAGGCTGC 1815
                                                                                                                                                                                                                                                                  Piplani S,
                                                                                                                                                       27-APR-2001; 2001WO-US13598.
                                                                                                                                                                                           28-APR-2000; 2000US-0561470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 TrpGlyProGluGlyCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.31e+07
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100.00%
0.87%
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                                                                                                                                                                                                                              (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                Chen M,
                                                                                                                                                                                                                                                                                               WPI; 2002-075158/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                   WO200183693-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                Schatz PJ,
                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nvention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR82184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match:
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from the group AAR82098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A melanoma-specific immunogen homologous with pMel-17 comprises one or more CTL (cytotoxic T lymphocyte) epitopes from the group AAR8209 AAR82194 capable of eliciting a CTL response. The epitopes AAR82098 AAR821098 are of particular interest. The immunogen can be used for partial protection in mammals against melanoma peptides which are homologous with pMel-17 are highly potent stimulators of HLA-A2+ cTLs in several cell lines and can be used in immunotherapy or incorporated into immunogenic conjugates as vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Metastatic melanoma; peptide analogue; vaccine; cancer; diagnosis; antigen; CTL; immunogenic; viral disease; gp 100; Melan A/MART-1.
                                                                                                                                                                                                                                                                                                                                                                    Melanoma-specific immunogen comprises epitope(s) homologous with pMel 17 - are highly potent stimulators of HLA-A2+CTL's useful in
                                                                                                                                                                                                                                                                                     Slingluff CL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         600000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Melan A/MART epitope (residues 27-35) analogue #5
                                                                                                                                                                                                                                                                                  Hunt DF, Shabanowitz J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
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                                                                                                                                                                                                                                       UYVI-) UNIN VIRGINIA PATENT FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 8; Page 52; 148pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1982 TTACAAGCTGCCATCCCC 1999
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6.00
                                                                                                                            95WO-US01991
                                                                                                                                                                                            94US-0197399
                                                                                                                                                                        94US-0234784
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                                                                                                                                                                                                                                                                                  Engelhard VH,
                                                                                                                                                                                                                                                                                                                                                                                                                  adoptive 1mmuno-therapy
                                                                                                                                                                                                                                                                                                                           WPI; 1995-302688/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
Homo sapiens
                                      W09522561-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo saptens.
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                                                                                                                            6-FEB-1995;
                                                                                                                                                                        39-APR-1994;
                                                                                                                                                                                            16-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38-JUL-1997;
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                                                                                 24-AUG-1995.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                  COX AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 19
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This sequence is shown in the specification. The invention relates to peptides, which are immunogenic with lymphocytes directed against metastatic melanomas. They are characterised in that they comprise at least a part of the following sequence, where the amino acid at position 2 or 8 is substituted: Lys-Thr-Trp-Gly-Gln-Tyr-Trp-Gly-Val. Vaccines comprising the peptide, an epitope of the peptide, nuclectide sequence encoding the peptide, or a antigen presenting cell preloaded with the peptide or antibody as above, are useful for cancer, particularly melanoma, treatment. The peptides can also be used to generate antigen reactive tumour infiltrating lymphocytes, which can also be used in reactive tumour infiltrating lymphocytes, which can also be used in reactive trace of the peptides can be exploited to elicit native epitope-reactive CTL. Usage of the peptides with improved immunogenicity may contribute to the development of CTL-epitope based vaccines in viral disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying agonists or antagonists for ligand-induced activation of
                                                                                    associated peptide analogues - useful in vaccines against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oestrogen receptor beta; ER-beta; MBP; binding; detection;
ligand-dependent nuclear receptor; coactivator interaction;
hybrid system; corepressor; ligand binding domain; LBD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Coactivator leucine charged domain peptide #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schatz PJ;
                                                                                                                                  Example 1; Page 28; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY42208 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-824-647-16 (1-2095) x AAW42528
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6.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.00%
100.00%
0.87%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Northrop JP, Hart CP,
(ALKU ) AKZO NOBEL NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-591374/50.
                              Figdor, CG;
                                                            WPI; 1998-110586/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Aliqnment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY42208;
                                 Adema GJ,
                                                                                            delanoma
                                                                                                          melanoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
                                                                                                                                                                                                                                                                                                                                                                      cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score:
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The present invention describes the use of a ligand binding domain (LBD) transcription factor (TRX) fusion protein in methods for identifying transcription factor (TRX) fusion protein in methods for identifying cranscription factor ligand-induced activation of a predetermined conclear receptor having a LBD. Also describes are: (1) a positive hybrid nuclear receptor signal transduction system, comprising an ideact comprising an ideact comprising a reverse hybrid reporter host cell; (3) a multipliexed format comprising a reverse hybrid reporter host cell; (3) a multipliexed format confider pharmaceutical agent from a library of test agents; (5) a candidate pharmaceutical agent from a library of test agents; (5) a confider pharmaceutical agent from a library of test agents; (5) a confider pharmaceutical agent from a library of test agents; (5) a confider pharmaceutical agent from a library of test agents; (5) a confider pharmaceutical agent from a library of test agents; (5) a confider pharmaceutical above methods are nuclear receptor, typically by interaction with a binding contring to ancelear receptor identified using above methods. The new methods are useful for identified using above methods. The new methods are cuseful for identified using above methods are lasting agonts to ligand-induced activation of a predetermined nuclear receptor having a LBD. The present sequence represents a coactivation lear invention in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; fung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
predetermined nuclear receptor having ligand binding domain (LBD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine; human leukocyte antigen; HLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-824-647-16 (1-2095) x AAY42208 (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1131 CTCCTCCGATACCTGCTG 1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY06031 standard; Peptide; 9 AA
                                                   Example 1; Fig 1; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98WO-US19609.
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6.00
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100.00%
0.86%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            used in an example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9918206-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 21
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RESULT 23
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   This peptide was identified as an HLA peptide motif following a screen for epitopes from the coding region of human ESO-1/CAG-3 ORF1 (see AAX5859). 30 Epitopes (see AAX60814-47) were identified.

The present peptide (ranked 14) corresponds to amino acid residues 153-160 of CAG-1 ORF1 (see AAX05965). CAG-1 is a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides (see AAX05967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer: cracked administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived concers such as primary or metastatic melanoma, thymoma, Imphoma, sarcoma, lung cancer, liver cancer, leuksemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocariomas such as breast, prostate, ovarian, pancreatic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
                                                                                                                                                                                                                                                                                                       690000
                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /accine; human leukocyte antigen; HLA
                                    Example 10; Page 43; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY06039 standard; Peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                             1119 CAGCAGCTGTCCCTCCTC 1136
                                                                                                                                                                                                                                                                                                                                                                                                                           2 GlnGlnLeuSerLeuLeu 7
            Cancer antigen NY ESO1/CAG-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cancer antigen NY ESO1/CAG-3
                                                                                                                                                                                                                                                                                                    2.94e+07
6.00
100.00%
100.00%
0.86%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-277270/23
                                                                                                                                                                                                                                                                                                                                       Best Local Similarity:
                                                                                                                                                                                                                                                                 9 AA;
                                                                                                                                                                                                                                           thyroid cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosenberg SA,
                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9918206-A2.
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                                                                                                                                                                                                                                                                                      Aliqnment Scores:
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                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY06039;
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                                                                                                                                                                                                                                                                                                     . No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 22
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screen for epitopes from the coding region of human ESO-1/CAG-3
C ORF1 (see AAX5659). 30 Epitopes (see AAX0618-47) were identified.
The present peptide (ranked 22) corresponds to amino acid residues
152-160 of CAG-1 ORF1 (see AAX05965). CAG-1 is a new and potent
tumour antigen capable of eliciting an antigen specific immune
response by T cells. Cancer peptides (see AAX05967-87) derived from
CAG-3, portions of CAG-3 and their variants, are useful as cancer
c vaccines. A claimed method of preventing or inhibiting cancer
involves administering a cancer peptide, with or without an HLA
molecule. The cancer peptides form part of, or are derived
from, cancers such as primary or metastatic melanoma, thymoma,
Iymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
cancer, cervical cancer, bladder cancer, leukaemia, uterine
cancer, cervical cancer, bladder cancer, kidney cancer and
adenocarcinomas such as breast, prostate, ovarian, pancreatic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; leukaemia; non-Hodgkins lymphona; Hodgkins lymphona; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; errical cancer; cancer; tuding cancer; tuding cancer; tuding cancer; cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy; vaccine; human leukocyte antigen; HLA.
                                                            This peptide was identified as an HLA peptide motif following a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60000
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (1-9)
Example 10; Page 43; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 10; Page 43; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY06025 standard; Peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1119 CAGCAGCTGTCCCTCCTC 1136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-824-647-16 (1-2095) x AAY06039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-277270/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thyroid cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rosenberg SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               domo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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DB:
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modulators of nuclear hormone receptor function, without the use of cell- or gel-based steps. The methods are amenable to automated, cost-effective high throughput screening of chemical libraries for bioactive compounds. To ensure specificity and optimize binding, the sensor is generally present at sub-micromolar concentration and the binding reaction occurs in solution. The sensor peptide obviates the need to include a natural coactivator protein of the receptor in the mixture. Sequences AR13571-587 represent examples of sensor peptides that can be used in the method of the invention.

9 AA;

Sequence

binding. The methods and compositions provide for efficient screening of

Nuclear hormone receptor; sensor peptide; receptor binding; screening; This peptide was identified as an HLA peptide motif following a screen for epitopes from the coding region of human ESO-1/CAG-3 ORF1 (see AAX58599). 30 Epitopes (see AAV06018-47) were identified. The present peptide (ranked 8) corresponds to amino acid residues 154-162 of CAG-1 ORF1 (see AAY05965). CAG-1 is a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides (see AAY05967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer involves administering a cancer peptides, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and 00000 Conservative: Mismatches: Indels: Length: Matches: Gaps: (1-9)AAY13578 standard; peptide; 9 AA. 1119 CAGCAGCTGTCCCTCCTC 1136 US-09-824-647-16 (1-2095) x AAY06025 GlnGlnLeuSerLeuLeu 6 98US-0163713. 97US-0975614. .94e+07 .00 98WO-US24969 100.00% 100.00% 0.86% 30-JUL-1999 (first entry) Peptide sensor IUK-1472 Best Local Similarity: Query Match: Sequence 9 AA; thyroid cancers. Percent Similarity: 20-NOV-1998; 30-SEP-1998; 21-NOV-1997; Alignment Scores: 03-JUN-1999 Synthetic. modulator AAY13578; .. 90 AAY13578 RESULT Score:

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The present invention describes a method of inducing and/or sustaining an immunological cytotoxic T lymphocyte (CTL) response in a mammal. The method comprises: (a) delivering an antigen to the mammal at a level to induce an immunological CTL response in the mammal; and (b) maintaining the level of the antigen in the mammal's lymphatic system to maintaining the immunologic CTL response. The method can be used for the delivery of e.g. a differentiation antigen, a tumour-specific multilineage antigen, an embryonic antigen, an oncogene antigen, a mutated tumour-suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of antigen in the lymphatic system of a mammal so as to provide a sustained CTL response, used to treat, e.g. AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytotoxic T-lymphocyte response; CTL; antigen; lymphatic system; immunisation; tumour; infectious disease; immunotherapy; cancer; malignant melanoma; viral disease; hepatitis; AIDS.
                                                                                                                                                                                690000
                                                                                                                                                                                                       Conservative:
Mismatches:
                                                                                                                                                                                Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLA Class I motif peptide SEQ ID NO:463.
                                                                                                                                                                                                                                                                          US-09-824-647-16 (1-2095) x AAY13578 (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 45; 199pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CTLI-) CTL IMMUNOTHERAPIES CORP.
                                                                                                                                                                                                                                                                                                                                                                                    AAY10533 standard; Peptide; 9 AA
                                                                                                                                                                                                                                                                                                    1131 CTCCTCCGATACCTGCTG 1148
                                                                                                                                                                                                                                                                                                                  1 LeuLeuArgTyrLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-0988320.
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                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-JUL-1997;
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                                                                                                                                                                    Aliqument Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                              AAY10533;
                                                                                                                                                                                                                                                                                                                                                                       AAY10533
                                                                                                                                                                                                                                                                                                                                                          RESULT
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hormone receptor function. The methods use a sensor peptide covalently coupled to a detectable label, that provides direct, in vitro ligand-dependent binding to a nuclear hormone receptor. Penels of predetermined or randomized candidate sensors are readily screened for receptor

The invention provides methods for screening of modulators of nuclear

Nuclear hormone receptor drug screens

Claim 7; Page 18; 29pp; English.

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Lustig

Chen J,

Baeuerle P, Beckmann H,

WPI; 1999-347794/29.

(TULA-) TULARIK INC.

Length: Matches:

2.94e+07 6.00

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100.00% 100.00% 0.86%

Percent Similarity: Best Local Similarity:

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disease such as cancer, e.g. malignant melanoma or infectious disease, e.g. viral disease such as hepatitis or ADDS. Sustained antigen delivery to the lymphatic system provides for potent CTL stimulation that takes place in the milleu of the lymphoid organ, and it sustains stimulation that takes that is necessary to keep CTL active, cytotoxic and recirculating through the body. AAV10071 to AAV1063 represent examples of peptide antigens given in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen; HLA; HLA binding peptide; major histocompatibility complex; MHC; tumour; cancer; testis tumour.
  They can be used for the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumour associated antigen EY-ESO-1 (LAGE-2) useful
                                                                                                                                                                                                                                                                                                                                                                                                                                       Cancer testis tumour antigen NY-ESO-1 derived peptide.
                                                                                                                                                                      Matches:
Conservative:
Mismatches:
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gene antigen, or a viral antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomic sequences of tumour associ
for diagnosing testicular tumours
                                                                                                                                                                                                                                                                                                                                                       AAG67189 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                            918 GGCCTGGGGCTGCTGCCC 935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                           22-FEB-2000; 2000US-0510635.
                                                                                                                                                         2.94e+07
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100.00%
0.86%
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                                                                                                                                                                                               Best Local Similarity:
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                                                                                                                                                                                  Percent Similarity:
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                                                                                                                                            Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                    AAG67189;
                                                                                                                    Sequence
                                                                                                                                                                                                              Query Match:
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individual that comprises determining the ratio of phospho-tau (181)/
total tau. Tau and phospho tau are useful as neurological markers for the
manufacture of a diagnostic kit for the diagnosis of a tauopathy and/or
the differential diagnosis of a tauopathy versus a non tauopathy. A
phospho-peptide liable to form an immunological complex with monoclonal
antibody HT7 and MAD AT270 comprising at least the minimal epitope of HT7
or AT270 is useful to measure phospho-tau levels and diagnose a tauopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phosphopeptide kits and methods are useful for therapeutic monitoring and for determining the effectiveness of a treatment. Sequences AAB85641-64 represent synthetic peptides immunoreactive to tau antibodies HT7, taul,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Tauopathy; phospho-tau (181); neurological marker; antibody; BT2; AT120;
BT7; AT270; nootropic; neuroprotective; cerobroprotective; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and/or for the differential diagnosis of a tauopathy versus a non
tauopathy. The kit is useful for the diagnosis of Alzheimer's disease,
Pick's disease, sporadic Frontotemporal dementia and/or Frontotemporal
dementia with Parkinsonism linked to chromosome 17, Creutzfeldt Jacob
disease, stroke and/or neurotoxicity in patients with leukemia. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Determining the ratio of phospho-tau / total tau is useful for diagnosing a tauopathy i.e. Alzheimer's disease or Pick's disease, versus a non tauopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention provides a method of diagnosis of tauopathies in an
                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic peptide immunoreactive with tau antibody HT7
60000
                              Conservative:
Mismatches:
Indels:
                                                                                                                                  US-09-824-647-16 (1-2095) x AAG67189 (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vanmechelen E, Vanderstichele H;
                                                                                                                                                                                                                                                                                       AAB85641 standard; peptide; 9 AA
                                                                                                                                                                       1119 CAGCAGCTGTCCCTCCTC 1136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Fig 1; 71pp; English.
                                                                                                                                                                                             GlnGlnLeuSerLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-JAN-2000; 2000EP-0870008.
27-JAN-2000; 2000US-0178391.
22-NOV-2000; 2000EP-0870280.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                               AAB85641;
                                                                         Query Match:
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Alignment Scores: Pred. No.:

bind to human leukcyte antigens (HLAs). NY-ESO-1 is a molecule that is processed to at least one human leukocyte antigen (HLA) binding peptide, which binds to Class I and Class II major histocompatibility complex (MHC). NY-ESO-1 is expressed in tumour mRNA and in testis, but not normal colon, kidney, liver or brain tissue. The presence or level of expression of NY-ESO-1 may be assayed for the diagnosis of cancer, especially testis tumours.

Alignment Scores:

Sequence

AAG67169-AAG67206 represent peptides which are derived from cancer testis tumour antigen NY-ESO-1 (also called LAGE-2). The peptides

Example 13; Page 26; 50pp; English.

Conservative: Mismatches:

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Length:
Matches:
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US-09-824-647-16 (1-2095) x AAU02257 (1-9)

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The invention provides a method of diagnosis of tauopathles in an individual that comprises determining the ratio of phospho-tau (181)/
c total tau. Tau and phospho tau are useful as neurological markers for the diagnostic kit for the diagnosis of a tauopathy and/or the differential diagnosis of a tauopathy versus a non tauopathy and/or phospho-peptide liable to form an immunological complex with monoclonal contibody HT7 and MAD AT270 comprising at least the minimal epitope of HT7 or AT270 is useful to measure phospho-tau levels and diagnose a tauopathy cand/or for the differential diagnosis of a tauopathy versus a non tauopathy. The kit is useful for the diagnosis of Alzheimer's disease, pick's disease, sporadic Frontotemporal dementia and/or Frontotemporal dementia and/or prototemporal dementia with Parkinsonism linked to chromosome 17, Creutzfeldt Jacob disease, stroke and/or neurotoxicity in patients with leukemia. The phosphopeptide kits and methods are useful for therapeutic monitoring and for determining the effectiveness of a treatment. Sequences ABBS661.64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tauopathy; phospho-tau (181); neurological marker; antibody; BT2; AT120;
BT7; AT270; nootropic; neuroprotective; cerobroprotective; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               represent synthetic peptides immunoreactive to tau antibodies HT7, taul,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Determining the ratio of phospho-tau / total tau is useful for diagnosing a tauopathy i.e. Alzheimer's disease or Pick's disease, versus a non tauopathy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic peptide immunoreactive with tau antibody HT7
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB85642 standard; peptide; 9 AA
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                                                                                                                                                                                     US-09-824-647-16 (1-2095) x AAB85641
                                                                                                                                                                                                                                           24-JAN-2000; 2000EP-0870008.
27-JAN-2000; 2000US-0178391.
22-NOV-2000; 2000EP-0870280.
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Query Match:
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                                                                                                                                                                                                                                                 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB85642;
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         Score:
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AAU02225-AAU02384 represent TADG-16 peptides which are tested for their binding affinity to the 8 haplotypes HLA A0201, HLA A0205, HLA A1, HLA A24, HLA B27, HLA B2702, and HLA B40203. Tumour antigen derived gene-16 protein, TADG-16 (AAU02223), is a novel human extracellular serine protease. TADG-16 (AAU02223), is a novel human conserved catalytic triad, His-Asp-Ser, and a signal secretion sequence characteristic of the serine protease family. An antisense oligonucleotide having a complementary sequence to the TADG-16 nucleic acid is useful for treating various cancers, including ovarian, breast, antibodies specific to TADG-16 nucleic acid, TADG-16 protein and antibodies specific to TADG-16 nucleic acid, TADG-16 protein and antibodies specific to TADG-16 are useful for the diagnosis of cancer.
                                                                                                                                                                                                                                                                                              Human; extracellular serine protease; tumour antigen derived gene-16; TAMG-16; ovarian carcinoma; breast cancer; lung cancer; colon cancer; prostate cancer; HLA type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New tumour antigen-derived gene-16 protein, useful for diagnosis and treatment of ovarian, breast, lung, colon and prostate cancer
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                                                                      US-09-824-647-16 (1-2095) x AAB85642 (1-9)
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                                                                                                                                                                                     AAU02257 standard; Peptide; 9 AA
                                                                                                                                                                                                                                                                         HLA binding TADG-16 peptide #33.
                                                                                                  GGGCAGCACCCCCAGGA 448
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Percent Similarity: 100.008
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Query Match: 0.878
                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                   AAU02257;
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AAU02360;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oligonucleotide having a complementary sequence to the TADG-16 nucleic acid is useful for treating various cancers, including ovarian, breast, lung, colon and prostate. The TADG-16 nucleic acid, TADG-16 protein and antibodies specific to TADG-16 are useful for the diagnosis of cancer. TADG-16 protein or tast fragments are useful for vaccinating an individual against TADG-16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMU0225-AAU02384 represent TADG-16 peptides which are tested for their binding affinity to the 8 haplotypes HLA A0201, HLA A0205, HLA A1, HLA A24, HLA B7, HLA B2702, and HLA B4403. Tumour antigen derived gene-16 protein, TADG-16 (AAV02223), is a novel human extracellular serine protease. TADG-16 is expressed in normal ovaries and testes and in certain ovarian carcinomas. TADG-16 contains the conserved catalytic triad, His-Asp-Ser, and a signal secretion sequence characteristic of the serine protease family. An antisense
                                                                                                                                                                                                              protease; tumour antigen derived gene-16; breast cancer; lung cancer; colon cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New tumour antigen-derived gene-16 protein, useful for diagnosis and treatment of ovarian, breast, lung, colon and prostate cancer -
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ID AAU02360 standard; Peptide; 9 AA.
                                                                                      AAU02355 standard; Peptide; 9 AA
                                                                                                                                                                             HLA binding TADG-16 peptide #131
884 GGGCAGCTCACCTCCATG 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; extracellular serine
TADG-16; ovarian carcinoma;
prostate cancer; HLA type.
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884
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                                                          RESULT 30
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oligonucleotide having a complementary sequence to the TADG-16 nucleic acid is useful for treating various cancers, including ovarian, breast, lung, colon and prostate. The TADG-16 nucleic acid, TADG-16 protein and antibodies specific to TADG-16 are useful for the diagnosis of cancer. TADG-16 protein or its fragments are useful for vaccinating an individual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU02225-AAU02384 represent TADG-16 peptides which are tested for their binding affinity to the 8 haplotypes HiA A0201, HIA A0205, HIA A1, HIA A24, HIA B7, HIA B8, HIA B2702, and HIA B4403. Tummour antigen derived gene-16 protein, TADG-16 (AAU02223), is a novel human extracellular serine protease. TADG-16 is expressed in normal ovaries and testes and in certain ovarian carcinomas. TADG-16 contains the conserved catalytic triad, HIS-ASP-Ser, and a signal secretion sequence characteristic of the serine protease family. An antisense
                                                                                           Human; extracellular serine protease; tumour antigen derivéd gene-16;
TADG-16; ovarian carcinoma; breast cancer; lung cancer; colon cancer;
prostate cancer; HLA type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New tumour antigen-derived gene-16 protein, useful for diagnosis and treatment of ovarian, breast, lung, colon and prostate cancer -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 8; Page 55; 124pp; English.
                                                      HLA binding TADG-16 peptide #136
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                                                                                                                                                                                                                                                                         WO200127257-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is given in a specification relating to a method for determining the status of a cancerous condition in a patient with a tumour that expresses NV-ESO-1. The method comprises assaying a sample taken from the patient for antibodies that specifically bind to the NY-ESO-1 and comparing the value obtained to a prior value obtained between the values is indicative of a change in status of the cancerous condition. The method is useful for determining whether a cancerous condition is progressing, remaining stable, in particular in patients receiving treatment for a melanoma, adenocarcinoma, non-small cell lung carcinoma or bladder carcinoma.
                                                                                                                                                                                                                                                                                                                                                         Method useful for determining the status (e.g. progression, regression or stability of the disease) of a cancerous condition, involves determining the levels of NY-ESO-1 specific antibodies in a sample
 Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell; HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma; non-small cell lung carcinoma; tumour status determination.
                                                                                                                                                                                                                                                                                             Scanlan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunogenic peptide with (HLA)-A2.1 binding site #16.
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                                                                                                                                                                                                                               (LUDW-) LUDMIG INST CANCER RES. (SLOK ) SLOAN KETTERING INST CANCER RES. (CORR ) CORNELL RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-824-647-16 (1-2095) x AAB69921 (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 14; Page 25; 50pp; English:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU95803 standard; Peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1119 CAGCAGCTGTCCCTCCTC 1136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                old LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlnGlnLeuSerLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.94e+07
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100.00%
0.86%
                                                                                                                                                                     14-JUL-2000; 2000WO-US19220.
                                                                                                                                                                                                 99US-0359503.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.00
                                                                                                                                                                                                                                                                                                  Stockert E,
                                                                                                                                                                                                                                                                                                                                                                                                               taken from a patient
                                                                                                                                                                                                                                                                                                                                WPI; 2001-182822/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 AA;
                                                                                                     MO200107917-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                         Homo sapiens
                                                                                                                                                                                                      23-JUL-1999;
                                                                                                                                       01-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU95803;
                                                                                                                                                                                                                                                                                                    Jager E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 33
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The invention describes a composition comprising an immunogenic peptide having a human leucocyte antigen (HLA)-A2.1 binding site. The peptides bind specifically to HLA-A2.1, to cause T cell activation and thus a cytotoxic T cell response. The peptides and the nucleic acids that encodes them, are used, in vivo or ex vivo, for treatment of viral infections (hepatitis B or C; Epstein-Barr; human immune deficiency; taxposi sarcoma; human papilloma; Lassa fever or cytomegaloviruses); tumours including prostate cancer, renal carcinoma and lymphona (where directed to prostate ancer, renal carcinoma and lymphona (where or melanoma antigene); infection by Mycobacterium tuberculosis or protozoa (directed to trypanosome surface antigen); and condlyloma accuminatum. The peptides are suitable for use in peptide based
cytomegalovirus; tumour; prostate cancer; renal carcinoma; lymphona; prostate-specific antigen; p53; carcino-embryonal antigen; melanoma antigen; Mycobacterium tuberculosis; protozoa; trypanosome surface antigen; condlyloma acuminatum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunogenic peptide with human leucocyte antigen-A2.1 binding site, useful for treating e.g. viral infection or tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vaccines. This sequence represents an immunogenic peptide with the human leucocyte antigen (HIA)-A2.1 binding site, described in the
                                                                                                                                                                                  Æ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New bradykinin analogue with D-beta-(2-napththyl)-Ala,
beta-(2-thienyl)-Ala and D-Phe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 690000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bradykinin analogue; bradykinin antagonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                ∵ is
                                                                                                                                                                                                                                                                                                                                                                                                                                    Southwood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-824-647-16 (1-2095) x AAU95803 (1-9)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ė
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 GGGACGCCAGCAGCTGTA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAP90829 standard; protein; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 24; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                    Grey HM, Sette A, Sidney J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlyThrAlaAlaAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.94e+07
6.00
100.00%
100.00%
0.87%
                                                                                                                                                                                                                                                                          01-SEP-2000; 2000WO-US24102.
                                                                                                                                                                                                                                                                                                                                  01-SEP-2000; 2000WO-US24102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JUN-1990 (first entry)
                                                                                                                                        Aycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                           (EPIM-) EPIMMUNE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-351766/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 AA;
                                                                                                                                                                                         WO200220616-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                           14-MAR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAP90829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAP90829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score:
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Si.:

Zoller MJ;

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The sequences given in AAR93272-342 represent peptides which are SH3
ligands/SH3 binding agents. They represent a biased phage library
which comprises ix random amino acids flanking the tetrapeptide
- PPIP which was identified as a recognition sequence for the src SH3
domain. These sequences were identified using the method of the
invention. The method comprises contacting the SH3 domain with a
mixture of peptides under conditions permitting a ligand to bind to
an SH3 domain to form a complex. Any unbound peptides are removed
an SH3 domain to form a complex. Any unbound peptides are removed
an SH3 domain and then candidates which bind to the SH3 domain are
SH3 domain and then candidates which bind to the SH3 domain are
detected. The isolated SH3 binding peptides may be used in the
dagnosis, prevention and treatment of conditions or diseases resulting
from cellular processes mediated by an SH3-based interaction. Such
diseases include Paget's disease. Other conditions treatable with these
peptides include restenosis, rheumatoid arthritis, gout and other
problems in which an SH3 of neutrophil oxidase P47 and p67 complex is
                                                                                                                                                                                                                                                                                           Identification of peptide(s) binding specifically to SH3 domains for use in inhibiting interactions mediated by SH3 domains in treatment of e.g. osteoporosis and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chlamydial epitope; variable domain; MOMP;
major outer membrane protein; picornavirus; poliovirus; PV1;
diagnostic; therapeutic; capsid protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels:
                                                                                                                                                                                                                    Rickles RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-824-647-16 (1-2095) x AAR93340 (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ź
                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 1; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1127 GTCCCTCCTCCGATACCT 1144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chlamydia trachomatis serovar A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR66370 standard; peptide; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 ValProProProllePro 10
                                                                                                                  95US-0369832.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.88e+04
6.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chlamydial MOMP VDI epitope.
                                                                             95WO-US03208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.00%
100.00%
0.86%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-JUN-1995 (first entry)
                                                                                                                                                                                                                  Brugge JS,
                                                                                                                                                                         PHARM INC
                                                                                                                                                                                                                                                        WPI; 1995-328231/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          implicated, etc.
                                                                                                                                                                             (ARIA-) ARIAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity
                                                                                                                  06-JAN-1995;
11-MAR-1994;
  W09524419-A1
                                                                           13-MAR-1995;
                                                                                                                                                                                                                  Botfield MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                        14-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9426900-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR66370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR66370
    It may be prepd. by conventional liq. - or solid-phase peptide synthesis methods. It is useful for treating local pain, inflammation and swelling, rhinitis, hypotension, asthma, arthritis, diarrhoea, irritable bowel syndrome, carcinoid syndrome, angina pain, and anaphylactic or septic shock. Pharmaceutical compsns. can be made with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SH3 ligand, SH3 binding agent; blased phage library; restenosis; recognition sequence, src SH3 domain; Paget's disease; restenosis; rheumatoid arthritis; gout; neutrophil oxidase; tyrosine kinase; p47; p67; complex; chronic myelogenous leukaemia; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New peptide bradykinin analogues -
with D-amino acid in 7 position, useful as bradykinin antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    00000
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TSK protein tyrosine kinase derived peptide #4.
                /note="D-beta-(2-naphthy1)-Ala
                                                                                                                                  'note="beta-(2-thienyl)-Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-824-647-16 (1-2095) x AAP90829 (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR93340 standard; peptide; 10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 10; page 52; 54pp; English.
                                                     /label=OTHER
/note="As above"
                                                                                                                                                                                           'note="As above"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             462 GCAGCACCCCAGGAGCC 445
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/label=OTHER
                                                                                                              /label=OTHER
                                                                                                                                                                                                                                  /label=D-Phe
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                                                                                                                                                                                                                                                                                                                                                                                           870S-0091995
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100.00%
0.87%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vavrek RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1989-085401/11
                                                                                                                                                                                                                                                                                                                                                                                                                                  (STEW/) STEWART JM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                  Misc-difference
                                                                                           Misc-difference
                                                                                                                                                    Misc-difference
                                                                                                                                                                                                          Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                       02-SEP-1987;
                                                                                                                                                                                                                                                                                                                                                  39-AUG-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
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                                                                                                                                                                                                                                                                     WO8901781-A.
                                                                                                                                                                                                                                                                                                              09-MAR-1989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stewart JM,
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Sequence

Pred

Query Match:

Synthetic

AAR93340;

RESULT 35 AAR93340

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Identifying compounds which interact with target molecules - using enantiomers of the target molecules and testing of enantiomers of selected compounds.
                                                                   Disclosure; Fig 8; 89pp; English.
WPI; 1997-480355/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW82826;
                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW82826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                       Mahoney CDNA clone PTXID was modified to encode epitopes from C. trachomatis ser. A MOMP VDI. The mutagenesis cartridge was contained between PV nucleotides 273-91 (given in AAQ79003) which encode PV amino acids 1022-1104 (AAR66375) which include the BC loop of capsid protein VPI (AAR66386). The pollo-specific DNA within the cartridge, encoding the sequence given in AAR66369, was replaced by oligonucleotides encoding VDI peptides AAR66370-74. Viable PV vero cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteriophage peptide library;peptide epitope; therapeutic target;
variegated compound library; interleukin-8; IL-8.
                                                                                                                                                        nseq
                                                                                                                                                        New hybrid picornaviruses expressing chlamydial epitopes - to develop prods. for vaccination, diagnosis, treatment of chlamydial infections and prodn. of immunological reagents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D-form Interleukin-8 peptide ligand consensus sequence 2.
                                                                                                                                                                                                                              obtain a poliovirus-1 (PV1)/chlamydial hybrid, the PV1
                                                                                                                                                                                                                                                                                                                                                                                              00000
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
Indels:
                                                                                                            Oomen RP;
                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-824-647-16 (1-2095) x AAR66370 (1-10)
                                                                                                            Klein MH, Murdin AD,
                                                                                                                                                                                                       Disclosure; Page 15; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW42311 standard; Peptide; 10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96US-0622338
                                       94WO-CA00262.
                                                                                                                                                                                                                                                                                                                                                                                               1.88e+04
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100.00%
0.86%
                                                             93US-0060978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                     (CONN-) CONNAUGHT LAB LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HARD ) HARVARD COLLEGE
                                                                                                                                    WPI; 1995-006796/01
                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                             10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09735194-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-MAR-1996;
                                                                                                            Caldwell HD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-APR-1998
                                       12-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                              3-MAY-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Forster AC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW42311;
                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW4231]
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The present sequence represents a consensus sequence obtained after several rounds of selection and amplification of a 6-mer peptide library. The consensus sequence is derived from peptide ligands of a D-enantiomer of interleukin-8 (IL-8), and was obtained using the method of the carget molecule, and comprises contacting a screening molecule with a variegated compround library, where the screening molecule with a target molecule, or the enantiomer if the target molecule as chiral. Compounds which have a desired interaction with the target molecule is called interaction with the target molecule are selected, and the ability of their enantiomer to interact with the target compounds which have a desired interaction with the target protein (a D-target protein), and a combining a D-panationer of a target protein (a D-target protein), and a variegated compound library, and then selecting one or more compounds to the library which have a desired binding interaction with the carget protein. The methods can be used for identifying agonists or at an analysis of target protein one with the carget protein. The methods can be used for identifying agonists or an analysis of target protein. The methods converse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antagonists of targets such as receptors, enzymes, DNA binding proteins or signal transduction proteins. The methods can provide a structurally selective approach in addition to scoring for interaction of functional groups. They provide a powerful selection method that allows for the production of ligands with the same diversity as peptides but with the greatly improved pharmacokinetic profiles needed for drug activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytomodulating lipophilic oligopeptide; immune system; inflammation; cytotoxic; lymphocytic; inhibition; cytokine; autoimmune disease; T (B cell; mononuclear phagocyte; septic shock; rheumatoid arthritis; Crohn's disease; colitis; allergy; transplant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     00000
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW82826 standard; peptide; 10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-824-647-16 (1-2095) x AAW42311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       741 GIGAICGGAGCAGCAGGT 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 ValileGlyAlaAlaGly 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SANG-) SANGSTAT MEDICAL CORP
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97US-0838916,
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6.00
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Best Local Similarity:
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11-APR-1997;
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us-09-824-647-16.lim.rag

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AAY06009
    AAW82804 to AAW82829 are cytomodulating lipophilic oligopeptides. The cligopeptides are used to inhibit: (1) activity of lymphocytes (particularly cytotoxic T cells, but also natural killers, B cells and monounclear phagocytes); (ii) production of inflammatory cytokines, and (iii) an inflammatory response in mammals (e.g. in cases of septic shock, rheumatory arthritis (RA), Crohn's disease, colitis and allergy). They are also used for modulating activity of haem-containing enzymes and for delaying onset of autoimmune disease (specifically insulin-dependent diabetes mellitus, RA and systemic lupus erythematosus). In all cases the oligopeptides may be generated from nucleic acids, and treatments are in vitro or in vivo. A specific application is treatment of organs or cells for transplantation, or of the recipient of such treansplants. Apart from therapeutic use, the oligopeptides can be used to study mechanisms of T cell (de)activation and to raise antibodies that are competitors of the oligopeptides. The oligopeptides are administered by bolus injection or infusion, typically at 0.1-50 (preferably 1-25)
                                                                   New lipophilic peptide(s) that inhibit activation of immune system cells - used for, e.q. production of cytokine(s) and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy; vaccine; human leukocyte antigen; HLA.
                                                                                  cells - used for, e.g. production of cytokine(s) and the inflammatory response, and also for modulating haem-containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                         Claim 7; Page 37; 48pp; English.
              Grassy G;
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              Calas
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                                                                                                                enzymes
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DB:
              Buelow
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coren for epitopes from the coding replan of human ESO-1/CAG-3

ORF1 (see AAX5859). 30 Epitopes (see AAV5988-Y06017) were identified.

The present peptide (ranked 12) corresponds to amino acid residues

152-161 of CAG-1 ORF1 (see AAY05965). CAG-1 is a new and potent
tumour antigen capable of eliciting an antigen specific immune
crasponse by T (cells. Cancer peptides (see AAV05967-87) derived from
CAG-3, portions of CAG-3 and their variants, are useful as cancer
vaccines. A claimed method of preventing or inhibiting cancer
involves administering a cancer peptide, with or without an HiA
molecule. The cancer peptides form part of, or are derived
from, cancers such as primary or metastatic melanoma, thymoma,
C momble of the cancer peptides form part of, or are derived
crack, cervical cancer, bladder cancer, leukaemia, uterine
cancer, cervical cancer, bladder cancer kidney cancer and
adenocarcinomas such as breast, prostate, ovarian, pancreatic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; netastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
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                                                                                                                                                                                                                                                                                                                                                                  this peptide was identified as an HLA peptide motif following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
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Mismatches:
Indels:
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Matches:
                                                         (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                                                                                      Example 10; Page 42; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY06009 standard; Peptide; 10 AA.
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                                                                                                                                                                                                                                             Cancer antigen NY ESO1/CAG-3
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6.00
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97US-0061428
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                                                                                                                     Wang RF
                                                                                                                                                                              WPI; 1999-277270/23.
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thyroid cancers
                                                                                                                  Rosenberg SA,
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08-OCT-1997;
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This peptide was identified as an HLA peptide motif following a screen for epitopes from the coding region of human ESO-1/CAG-3 ORF1 (see AAX5859). 30 Epitopes (see AAX5898-Y06017) were identified. The present peptide (ranked 22) corresponds to amino acid residues 154-163 of CAG-1 ORF1 (see AAX05965). CAG-1 is a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides (see AAX05967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
                                                                                                                                                                                                                                                                                                                involves administering a cancer peptide, with or without an Hish molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastetic melanoma, lympoma, lymphoma, sarcoma, lung rancer, luver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                00000
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Conservative:
Mismatches:
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              (USSH ) US DEPT HEALTH & HUMAN SERVICES
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                                                                                                                                          Example 10; Page 42; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY05997 standard; Peptide; 10 AA.
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                                                                                                          Cancer antigen NY ESO1/CAG-3
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                                            Rosenberg SA, Wang RF;
                                                                         WPI; 1999-277270/23.
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                     thyroid cancers.
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DB:
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ID AAX
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This peptide was identified as an HLA peptide motif following a screen for epitopes from the coding region of human ESO-1/CAG-3 coren for epitopes (see AAY0598-706017) were identified.

CORFI (see AAX5859) 30 Epitopes (see AAY0598-706017) were identified.

The present peptide (ranked 10) corresponds to amino acid residues to manno acid residues and the present peptide (ranked 10) carresponds to amino acid residues (see AAY05965).

CAG-1 ORFI (see AAY05965). CAG-1 is a new and potent tumour antigien capable of eliciting an antigen specific immune response by T cells. Cancer peptides (see AAY05967-87) derived from cag-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer involves administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived concerts such as primary or metastatic melanoma, thymoma, important or lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, liver cancer, kidney cancer and cancer acid cancer, prostate, ovarian, pancreatic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nuclear hormone receptor; sensor peptide; receptor binding; screening; modulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen J, Lustig K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nuclear hormone receptor drug screens
                                                                                                                                   Example 10; Page 42; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY13579 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGCAGCTGTCCCTCCTC 1136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0163713.
97US-0975614.
                                                                                             Cancer antigen NY ESO1/CAG-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.88e+04
6.00
100.00%
100.00%
0.86%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Baeuerle P, Beckmann H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide sensor TUK-1473.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TULA-) TULARIK INC.
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                                                      WPI; 1999-277270/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thyroid cancers.
                  Rosenberg SA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-SEP-1998;
21-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 42
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hormone receptor function. The methods use a sensor peptide covalently coupled to a detectable label, that provides direct, in vitro ligand-dependent binding to a nuclear hormone receptor. Panels of predetermined or randomized candidate sensors are readily screened for receptor binding. The methods and compositions provide for efficient screening of modulators of nuclear hormone receptor function, without the use of cell- or gel-based steps. The methods are amenable to automated, cost-effective high throughput screening of chemical libraries for bloactive compounds. To ensure specificity and optimize binding, the sensor is generally present at sub-micromolar concentration and the binding reaction occurs in solution. The sensor peptide obviates the need to include a natural coactivator protein of the receptor in the mixture. Sequences having the examples of sensor peptides that can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bacteria; fungi; yeast; protozoa; virus; mycoplasma; filaria; plasmodia;
infection; inflammation; microbial induced tumour; degenerative disorder
diarrhoea; colic; oral microflora; intestinal microflora; caries;
                                                screening of modulators of nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes milk-derived bifidogenic peptides and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bifidogenic peptide; protease; treatment; microbe-related disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Milk-derived peptides that stimulate Bifidobacterium bifidus
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Mismatches:
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Matches:
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                                               The invention provides methods for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW93872 standard; peptide; 10 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1131 CTCCTCCGATACCTGCTG 1148
             Claim 7; Page 18; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-824-647-16 (1-2095) x AAY13579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Page 3; 25pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-EP05899
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97DE-1040604.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaginal microflora.
                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                        10 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09914231-A2
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                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match:
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chemical coupling. Such are produced from bovine or human milk by treatment for 2 hr with proceases, then centrifuging to remove fat and aciditying to PH 2 to precipiate proteins. The solution phase is then subjected to reverse-phase high-performance liquid chromatography (HPLC) and cation-exchange HPLC, the fractions adjusted to salt content below to 55 mM (by dialysis or reverse-phase HPLC) and tested for activity by growing Bifidobacterium bifidus and Escherichia coli in pregence of the fractions. Those fractions for which (Bw-B0)-(Ew-EO) is at least 0.15 are selected where Bw = germ count after 16 hr culture of B. Difidus in 50 Biliker broth containing peptide at 0.2 mg/ml, BO = germ count after 16 hr culture of B. Difidus in 20 Biliker broth containing peptide free control. Ew = germ count after 16 hr culture of B. Difidus in 20 mg/ml, EO = germ count under similar conditions in a peptide-free control. The peptides AAW93865-W93888 are used to treat microbe-related diseases caused by bacteria, fundi, yeast, protozoa, viruses, mycoplasma, fillaria and plasmodia, eq. infections, inflammation, microbially induced tumours or degenerative disorders, diarrhoea, collc, abnormalities in oral, intestinal or vaginal microflora, or carles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Variable domain; MOMP; major outer membrane protein; subunit vaccine; C. trachomatis infection; serotyping; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents an epitope of the major outer membrane protein (MOMP) of Chlamydia trachomatis. The invention relates to variable domain fragments of the MOMP of Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chlamydia trachomatis peptides - and DNA fragments encoding them
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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920S-0853359
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-MAR-1992;
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16-MAR-1992;
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Cancer testis tumour antigen; NY-ESO-1; LACE-2; human leukocyte antigen; HLA; HLA binding peptide; major histocompatibility complex; MHC; tumour; cancer; testis tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genomic sequences of tumour associated antigen EY-ESO-1 (LAGE-2) useful for diagnosing testicular tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG67169-AAG67206 represent peptides which are derived from cancer testis tumour antigen NY-ESO-1 (also called LAGE-2). The peptides bind to human leukocyte antigens (HLAA). NY-ESO-1 is a molecule that is processed to at least one human leukocyte antigen (HLA) binding peptide, which binds to Class I and Class II major histocompatibility complex (MHC). NY-ESO-1 is expressed in tumour mRNA and in testis, but not normal colon, kidney, liver or brain tissue. The presence or level of expression of NY-ESO-1 may be assayed for the diagnosis of cancer, especially testis tumours.
           serovar I, serovar J, serovar K, and serovar LJ, and to DNA sequences encoding them. The peptides are useful in diagnostic tests for C trachomatis infections, serological tests for serotyping, and as subunit vaccines.
 serovar Ba, serovar D, serovar E, serovar F, serovar G, serovar H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cancer testis tumour antigen NY-ESO-1 derived peptide.
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Matches:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                          1279 GTGGCTGGACTGGAGAG 1296
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Query Match:
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Percent Similarity:
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Pred. No.:
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Best Local Similarity: 100.00% Mismatches: 0 Ouery Match: 0.86% Indels: 0 DB: 22 Gaps: 0
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US-09-824-647-16 (1-2095) x AAG67204 (1-10)

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Search completed: July 7, 2003, 16:07:23 Job time : 94 secs us-09-824-647-16.lim.rapb

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Sequence 5, Appli
Sequence 18, Appli
Sequence 143, Appli
Sequence 15, Appli
Sequence 7, Appli
Sequence 195, App
Sequence 5, Appli
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Sequence 7, Application US/09824647

Publication No. US20020183270A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996.488/P001-A

CURRENT APPLICATION NUMBER: US/09/824,647

CURRENT PILING DATE: EARLIER FLLING DATE: 1998-08-17

PRIOR APPLICATION NUMBER: EARLIER RAPLICATION NUMBER: 08/963,862

PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-23
                                                                                                                                         Sequence 55,
Sequence 375
Sequence 379
Sequence 389
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OTHER INFORMATION: Internal peptide of human GP88 used to develop
OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody
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0 US-09-824-807-5

US-09-864-46A-143

US-09-79-148-5

US-09-731-449-55

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US-09-731-449-55

US-09-731-449-55

US-09-572-404B-379

US-09-572-404B-403

US-09-572-404B-403

US-09-572-404B-403

US-09-572-404B-419

US-09-572-404B-200

US-09-572-404B-2101

US-09-572-404B-2101

US-09-572-404B-2101

US-09-572-404B-2101

US-09-572-404B-2101

US-09-572-404B-2103

US-09-572-404B-2103

US-09-572-404B-326

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US-09-572-404B-367

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 NAME/KEY: PEPTIDE
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-Q--C9012_1/INZPPO_gpool/T05984647/zunat_07072003_154800_26675/app_guery.fasta_1.2247
-Q--C9012_1/INZPPO_gpool/T05984647/zunat_0707213_11m.rapp.-MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS-bits -START=1 -END-1 -MATRIX-01150
-TRANS-humand10.cd1 _LIST-45 -DOCALIGN-200 -TRENSCORES=0 -MINLEN-15
-USER-US09824647_CGGL_1_124_erunat_07072003_154800_26675 -NCPG-6 -ICPU-3
-NO_MADP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-FGAPOPT-120 -WARN_TIMEOTY=30 -THRANS-1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP-60 -YGAPEXT=60 -DELOP=6 -DELEXT=7
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6257.407 Million cell updates/sec
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/cgn2_6/ptcdata/1/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptcdata/1/pubpaa/NS06_NEW_PUB.pep:*
/cgn2_6/ptcdata/1/pubpaa/US06_NEW_PUB.pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                    protein search, using frame_plus_n2p model
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US-10-218-509-7
US-10-281-160-7
US-09-813-156-7
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ORGANISM: Human granulin FEATURE:
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Best Local Similarity:
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NAME/KEY: PEPTIDE
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US-09-824-807-7
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Publication No. US20030108950A1
GENERAL INFORMATION:
APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REPERENCE: 2996.488/P001-A
CURRENT APPLICATION NUMBER: US/10/281,160
CURRENT PILING DATE: 2002-10-28
                                                                                                                                                                                                                                                                                      PEDELICANT: Serretco, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REPERENCE: 299964.488/P001-A
CURRENT APPLICATION NUMBER: US/10/218,509
CURRENT FILING DATE: 2002-08-15
PRIOR PELLING DATE: 1998-08-17
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver: 2.0
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monoclonal antibody
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OTHER INFORMATION: Internal peptide of human GP88
OTHER INFORMATION: neutralizing anti-human GP88 mo
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Matches:
Conservative:
Mismatches:
Indels:
                                    Conservative:
Mismatches:
Indels:
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      Length:
Matches:
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PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 08/863,862
PRIOR FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
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Query Match:
                                     Percent Similarity:
Best Local Similarity:
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NAME/KEY: PEPTIDE
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US-10-281-160-7
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SEQ ID NO 7
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Sequence 7, Application US/09824807
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Sequence 7, Sequen
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APPLICANT: SETION: Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996.488/P001-A
CURRENT APPLICATION NUMBER: US/09/813,156
CURRENT FILING DATE: 1997-12-16
PRIOR APPLICATION NUMBER: 08/991,862
PRIOR RILING DATE: 1997-12-16
PRIOR FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 14
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OTHER INFORMATION: Internal peptide of human GP88 used to develop
OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody
                                                                        GP88 used to develop
988 monoclonal antibody
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Matches:
Conservative:
Mismatches:
Indels:
NAME/KEY: PEPTIDE

LOCATION: (1)..(14)

OTHER INFORMATION: Internal peptide of human GP8

OTHER INFORMATION: neutralizing anti-human GP89

US-10-281-160-7:
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Matches:
Conservative:
Mismatches:
Indels:
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Patent No. US20020061859A1
GENERAL INFORMATION:
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FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(14)
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                                                                                                                                                                                         NAME/KET: PEPTIDE

LOCATION: (1)..(14)

COTHER INFORMATION: Internal peptide of human GP88 used to develop

COTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody.
US-09-824-807-7
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Patent No. US20020164668A1
GENERAL INFORMATION:
APPLICANT: Durham, L. Kathryn
APPLICANT: Friedman, David L.
APPLICANT: Herath, Herath, Mudiyanselage Athula Chandrasiri
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TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and TITLE OF INVENTION: Uses Therefor, Including Diagnosis and TITLE OF INVENTION: Alzheimer's Disease FILE REFERENCE: 2572-1-001 NZ Alzheimer's Disease CURRENT FILING DATE: 2001-04-30
PRIOR RAPLICATION NUMBER: US 60/194,504
PRIOR APPLICATION NUMBER: US 60/194,504
PRIOR APPLICATION NUMBER: US 60/253,647
PRIOR FILING DATE: 2000-04-03
PRIOR FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 492
SEQ ID NO 195
LENGTH: 14
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Matches:
Conservative:
Mismatches:
Indels:
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Conservative:
Mismatches:
Indels:
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PRIOR APPLICATION NUMBER: 08/991,862
PRIOR FILING DATE: 1997-12-16
PRIOR PILING DATE: 1997-12-16
PRIOR FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 7
LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kimmel, Lida H.
Parekh, Rajesh Bhikhu
Potter, David M.
Rohlff, Christian
Silber, B. Michael
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Sunderland, P. Trey
Townsend, Robert Reid
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1.01$
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100.00$
100.00$
2.02$
                                                                                                                                                         TYPE: PRT ORGANISM: Human granulin
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US-09-826-290-195
                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Ouery Match:
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Best Local Similarity:
Query Match:
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Sequence 5, Application US/10218509
; Publication No. US20030092661A1
; GENERAL INFORMATION:
APPLICANT: Serrero Ginette
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 30996.488/P001-A
; CURRENT APPLICATION NUMBER: US/10/218,509
; CURRENT FILING DATE: 1209-08-15
; PRIOR PILING DATE: 1999-08-17
; PRIOR FILING DATE: 1999-08-17
; PRIOR FILING DATE: 1999-05-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver: 2.0
; SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (1)..(14)
OTHER INFORMATION: Internal peptide of mouse GP88 used to raise the OTHER INFORMATION: antisera against the GP88 used in the OTHER INFORMATION: immunoaffinity step.
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Matches:
Conservative:
Mismatches:
US-09-824-647-16 (1-2095) x US-09-826-290-195 (1-14)
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                              1009 GGTACCTGTGAACAGGGGCCC 1029
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                                             1 GlyThrCysGluGlnGlyPro 7
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Best Local Similarity:
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NAME/KEY: PEPTIDE
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Query Match:
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Sequence 5, Application US/09813156
Patent No. US20020061859A1
GENERAL INFORMATION:
APPLICANT: Serrero, Ginette
APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REPERENCE: 29996.488/PP001-A
CURRENT PILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (1)..(14)
OTHER INFORMATION: Internal peptide of mouse GP88 used to raise the OTHER INFORMATION: antisera against the GP88 used in the OTHER INFORMATION: immunoaffinity step.
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Publication No. US20030108950a1
GENERAL INFORMATION:
APPLICART: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILLE REPERENCE: 29996.488/P001-A
CURRENT APPLICATION NUMBER: US/10/281,160
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION UNMER: US/08/991,862
PRIOR PILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 09/863,862
OTHER INFORMATION: Internal peptide of mouse GP88 used to raise the OTHER INFORMATION: antisera against the GP88 used in the OTHER INFORMATION: immunoaffinity step.
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Matches:
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Mismatches:
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PRIOR APPLICATION NUMBER: 08/991,862
PRIOR FILING DATE: 1997-12-16
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NUMBER OF SEQ ID NOS: 17
SOFFWARE: Patentin Ver. 2.0
SEQ ID NO 5
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1.01%
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Best Local Similarity:
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Best Local Similarity:
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US-09-824-807-5

Sequence 5, Application US/09824807

Patent No. US20020094966A1

GENERAL INFORMATION:

APPLICART: Seriero, Ginette

TITLE OF INVENTION: BERNA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS

TITLE OF INVENTION: L. S9996.488/P001-A

CURRENT APPLICATION NUMBER: US/09/824,807

CURRENT ALING DATE: 2001-04-04

PRIOR FILING DATE: 1997-12-16

PRIOR FILING DATE: 1997-12-16

PRIOR FILING DATE: 1997-05-23

NUMBER OF SEQ ID NOS: 17
                                                                                                                                     FEATURE:
| NAME/KEY: PETIDE | COATION: (1)...(14) | COATION: (1)...(14) | OTHER INFORMATION: Internal peptide of mouse GP88 used to raise the OTHER INFORMATION: antisera against the GP88 used in the OTHER INFORMATION: immunoaffinity step.
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NAME/KEY: PEPTIDE
LOCATION: (1)...(14)
OTHER INFORMATION: Internal peptide of mouse GP88 used to raise the OTHER INFORMATION: antisera against the GP88 used in the USHER INFORMATION: immunoaffinity step.
US-09-824-807-5
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Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
Indels:
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PRIOR APPLICATION NUMBER: 08/863,862
PRIOR FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 14
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                                                                                                       TYPE: PRT 'ORGANISM: mouse granulin
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Best Local Similarity:
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Query Match:
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DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED PROTEIN TAU, HYBRIDOMAS SECRETING THESE ANTIBODIES, ANTIGEN RECOGNITION BY THESE
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                                                                                                                                                                                                                                                                            VAN DE VOORDE, ANDRE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 27-JUN-1994
APPLICATION NUMBER: 08/256,167
FILING DATE: 13-JUN-1994
APPLICATION NUMBER: 08/244,951
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: PCT/EP93/03499
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APPLICATION NUMBER: EP/92/403403.6
FILING DATE: 14-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.003-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/790,148
FILING DATE: 21-Feb-2001
PRIOR APPLICATION DATA:
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ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE DESCRIPTION: SEQ ID NO: 5:
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NAME: CHARLES A. MUSERLIAN
                                                                                                                                                                                                                                   MERCKEN, MARC;
VANMECHELEN, EUGEEN;
                                                                                                                        % Sequence 5, Application US/09790148
; Sequence 5, Application US/09790148
; Patent No. US20020001857A1
; GENERAL INFORMATION:
APPLICANT: VANDERMEREN, MARC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELEPHONE: (212) 661-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: FLOPPY DISK
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                          1638 CTGCTGTCCCTACGCCCA 1655
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SEQUENCE CHARACTERISTICS
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6.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 10016
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Query Match:
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                                                                                                             RESULT 14
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                                                                                                  APPLICANT: Beer, Ilan
APPLICANT: 21v, Tamar
APPLICANT: Admon, Arie
TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECULE
TITLE OF INVENTION: PEPTIDES IDENTIFIED THEREBY AND THEIR USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Peptide with peptide binding sequence retrieved from phage biopar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Belcher, Angela M
APPLICANT: Smalley, Richard E.
APPLICANT: Smalley, Richard E.
APPLICANT: Ryan, Esther
APPLICANT: Lee, Seung-Wuk
TITLE OF INVENTION: BIOLOGICAL CONTROL OF NANOPARTICLES
FILE REFERENCE: 119927-1066
CURRENT APPLICATION NUMBER: 05/10/254,446A
CURRENT FILICATION NUMBER: 60/325,664
PRIOR FILING DATE: 2001-09-28
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Matches:
Conservative:
Mismatches:
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Conservative
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                                                                                                                                                                                                      FILE REFERENCE: 01/22080
CURRENT APPLICATION NUMBER: 05/09/865,548A
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 05 60/290,958
PRIOR FILING DATE: 2001-05-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps:
                   Sequence 108, Application US/09865548A Publication No. US20030096298A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 143, Application US/10254446A Publication No. US20030113714A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: synthetic peptide US-09-865-548A-108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           459 CTGCCCCATGCCCCAGGC 476
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SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 204
SOFTWARE: Patentin version 3.1
SEQ ID NO 108
LENGTH: 9
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Query Match:
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US-09-865-548A-108
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FEATURE:

OTHER INFORMATION: sequence located in NPR3 OR ANPRC at 34-43 and may interact;

OTHER INFORMATION: Sequence 390 in this patent.

US-09-572-404B-389
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US-05-572-404B-389
US-06-572-404B-389
Sequence 389, Application US/09572404B
Sequence 389, Application US/09572404B
Sequence 389, Application US-0030078374Al
SEMERAL INFORMATION:
COMPENT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome FILE REFERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SEQ ID NO 389
SEQ ID NO 389
LENGTH: 10
                                                NGS-09-572-404B-379
Sequence 379, Application US/09572404B
Sequence 379, Application US/09572404B
Sequence 379, Application No. US20030078374A1
FURDILGANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome
TITLE REPERENCE: Human page: US/09/572,404B
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT PILING DATE: 2000-05-17
NUMBER OF SEQITO NOS: 4203
SOFTWARE: ProtPatent version 1.0
SEQ ID NO 379
LENGTH: 10
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Mismatches:
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ORGANISM: Homo Sapiens
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Query Match:
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Best Local Similarity:
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                                                                                                                                    PAPLICANT: Busfield, Samantha J.

PILLE OF INVENTION: NOVEL SECRETED IMMUNOMODULATORY PROTEINS AND USES THEREOF
FILE REFERENCE: 07334-320001.

CURRENT APPLICATION NUMBER: US/09/731,449

CURRENT FILING DATE: 1999-09-30

PRIOR APPLICATION NUMBER: US 09/410,350

PRIOR APPLICATION NUMBER: US 09/163,523

PRIOR FILING DATE: 1999-09-30

NUMBER OF SEQ ID NOS: 62

SOFTWARE: FESSERE for Windows Version 4.0

SEQ ID NO 55

LENGTH: 10
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TITLE OF INVENTION: Complementary peptide ligands from the human genome FILE REFERENCE: Human patent CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: Proteatent version 1.0
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Mismatches:
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
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                                                           US-09-731-449-55;
; Sequence 55, Application US/09731449
; Patent No. US20020155526A1
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        1 GlyAlaAlaProProGly 6
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ORGANISM: Homo Sapiens
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Best Local Similarity:
Query Match:
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Query Match:
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, VAREK INFORMATION: Sequence located in MPR3 OR ANPRC at 33-42 and may interact CTHER INFORMATION: Sequence 416 in this patent.
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                         APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome
FILE REFERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SEGTHARE: ProtPatent version 1.0
SEQ ID NO 415
LENGTH: 10
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Sequence 419, Deplication No. US20030078374A1

GENERAL INFORMATION.

APPLICANT: Proteom Ltd

TITLE OF INVENTION: Complementary peptide ligands from the human genome FILE REPERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B

CURRENT FILING DATE: 2000-05-17

NUMBER OF SEQ ID NOS: 4203

SOFTWARE: ProtPatent version 1.0

SEQ ID NO 419
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Mismatches:
Indels:
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Best Local Similarity: 100.00%
Query Match: 0.87%
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FEATURE:
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Best Local Similarity:
Query Match:
   GENERAL INFORMATION:
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US-09-572-404B-409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHER INFORMATION: sequence located in NPR3 OR ANPRC at 33-42 and may interact with COTHER INFORMATION: Sequence 404 in this patent.

US-09-572-404B-403
                                                                                                                   APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome
FILE REFERENCE: Human patent
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEO ID NOS: 4203
SOFTWARE: ProtPatent version 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 409, Application US/09572404B
| Sequence 409, Application US/09572404B
| Publication No. US20030078374A1
| GENERAL INFORMATION:
| APPLICANT: Proteom Ltd
| TILLE OF INVENTION: Complementary peptide ligands from the human genome
| FILE REFERENCE: Human patent
| CURRENT PAPLICATION NUMBER: US/09/572,404B
| CURRENT FILING DATE: 2000-05-17
| NUMBER OF SEQ ID NOS: 4203
| SOFTWARE: ProtPatent version 1.0
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Matches:
Conservative:
Mismatches:
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                         Sequence 403, Application US/09572404B Publication No. US20030078374A1 GENERAL INFORMATION:
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Query Match:
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US-09-572-404B-403
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LENGTH: 10
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Query Match:

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; OTHER INFORMATION: sequence located in ITPKB at 1964-1973 and may interact with cother information: 1059 in this patent.

US-09-572-404B-1060
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US-09-572-404B-2096
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Title OF INVENTION: Complementary peptide ligands from the human genome FILE REFERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SEPTAMEE: ProtPatent version 1.0
SEQ ID NO 2096
LENGTH: 10
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TITLE OF INVENTION: Complementary peptide ligands from the human genome
FILE REFERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProtPatent version 1.0
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NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProtPatent version 1.0
SEQ ID NO 1060
LENGTH: 10
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US-09-572-404B-502
                                                                                                                                                                                                        sequence located in PTHR1 OR PTHR at 271-280 and may interact wit Sequence 499 in this patent.
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Publication No. US20030078374A1
GENERAL INFORMATION.
APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome
FILE REPERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProtPatent version 1.0
SEQ ID NO 502
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Publication No. US20030078374A1
GENERAL INFORMATION:
APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome FILE REFERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
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      FILE REFERENCE: Human patent
CURRENT PAPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProtPatent version 1:0
SEQ ID NO 500
LENGTH: 10
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US-09-572-404B-500
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Best Local Similarity:
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US-09-572-404B-1060
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Pred. No.:
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; OTHER INFORMATION: sequence located in DDIT1 OR GADD45 at 104-113 and may in 1. OTHER INFORMATION: Sequence 3063 in this patent.
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                       sequence located in GUCY2D OR GUC2D OR RETGC1 OR RETGC OR CORD6 at 713-722 and may interact with Sequence 2774 in t
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Publication No. US20030078374A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome
TITLE OF INVENTION: Complementary peptide ligands from the human genome
TITLE REPERBNCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SSOFTWARE: Proteatent version 1.0
SSQ ID NO 3256
LENGTH: 10
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TITLE OF INVENTION: Complementary peptide ligands from the human genome FILE REPERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: Protpatent version 1.0
SEQ ID NO 3064
LENGTH: 10
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ORGANISM: Homo Sapiens
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                       CTHER INFORMATION:
CTHER INFORMATION:
US-09-572-404B-2773
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Query Match:
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US-09-572-404B-3256
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                                                                                ) OTHER INFORMATION: sequence located in CNTFR at 323-332 and may interact with Sequence OCHER INFORMATION: in this patent.
US-09-572-4048-2101
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OTHER INFORMATION: in this patent.
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TITLE OF INVENTION: Complementary peptide ligands from the human genome
TITLE OF INVENTION: Complementary peptide ligands from the human genome
TITLE REPERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProtPatent version 1.0
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APPLICANT: PROTECTION:
TITLE OF INVENTION: Complementary peptide ligands from the human genome FILE REPERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
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Sequence 2103, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
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                     TYPE: PRT
ORGANISM: Homo Sapiens
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ORGANISM: Homo Sapiens
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Query Match:
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Best Local Similarity:
Query Match:
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LENGTH: 10
LENGTH: 10
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; OTHER INFORMATION: sequence located in PKD1 at 316-325 and may interact with S.; CTHER INFORMATION: in this patent.
US-09-572-404B-3586
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TITLE OF INVENTION: Complementary peptide ligands from the human genome
FILE REFERENCE: Human patent
                                                                                                                                                                                                                                                                                                                                   APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTHER INFORMATION: sequence located in AVP OR ARVP OR VP at 87-96; OTHER INFORMATION: Sequence 3261 in this patent.
US-09-572-4048-3262
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Matches:
Conservative:
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProtPatent version 1.0
SEQ ID NO 3262
LENGTH: 10
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                                                                                                                                                                                                                                                                         Sequence 3262, Application US/09572404B Publication No. US20030078374A1 GENERAL INFORMATION:
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                                           Percent Similarity:
Best Local Similarity:
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Percent Similarity:
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DB:
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Score:
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: OTHER INFORMATION: 3257 in this patent.
US-09-572-404B-3258
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US-09-572-404B-3260
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TITLE OF INVENTION: Complementary peptide ligands from the human genome
FILE REFERENCE: Human particulus.
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProtPatent version 1.0
SEQ ID NO 3260
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Proteom Ltd
TILLE OF INVENTION: Complementary peptide ligands from the human genome
FILE REPERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SEG ID NO 3258
LENGTH: 10
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Matches:
Conservative:
Mismatches:
Indels:
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Sequence 3258, Application US/09572404B
Publication No. US20030078374A1
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Best Local Similarity:
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Best Local Similarity:
Query Match:
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               JS-09-572-404B-3256
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Alignment Scores:

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sequence located in Unknown at 96\text{--}105 and may interact will 3675 in this patent.
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US-09-572-404B-3675
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TTLE OF INVENTION: Complementary peptide ligands from the human genome
FILE REFERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProtPatent version 1.0
SEQ ID NO 3675
                                                                                                                                                                                                                                     APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome
FILE REPERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProtPatent version 1.0
SEQ ID NO 3674
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                      US-09-824-647-16 (1-2095) x US-09-572-404B-3673 (1-10)
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Mismatches:
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Mismatches:
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                                                              1042 AGGGCACCTGGTGGGGCC 1025
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                                                                             3 ArgAlaProGlyGlyAla 8
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ORGANISM: Homo Saplens
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OTHER INFORMATION:
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Best Local Similarity:
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; OTHER INFORMATION: 3672 in this patent.
US-09-572-404B-3673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence located in Unknown at 95-104 and may interact with Seque 3673 in this patent.
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TILLE OF INVENTION: Complementary peptide ligands from the human genome
TILLE REPERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
CURRENT FILING DATE: 2000-05-17
SOFTWARE: ProtPatent version 1.0
SEQ ID NO 3672
LENGTH: 10
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TITLE OF INVENTION: Complementary peptide ligands from the human genome FILE REFERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEC ID NOS: 4203
SOFTWARE: ProtPatent version 1.0
                                                                             US-09-824-647-16 (1-2095) x US-09-572-404B-3586 (1-10)
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Matches:
Conservative:
Mismatches:
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Indels:
Gaps:
Mismatches:
Indels:
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Best Local Similarity: 100.00%
Query Match: 0.86%
DB: 9
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ORGANISM: Homo Sapiens
FEATURE:
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Best Local Similarity:
Query Match:
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CTHER INFORMATION:
US-09-572-404B-3672
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Best Local Similarity:
Query Match:
DB:
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APPLICANT: Cerotini, Jean-Charles
APPLICANT: Cerotini, Jean-Charles
APPLICANT: Romero, Pedro
TITLE OF INVENTION: Isolated No. US20030082804Ala - And Decapeptides Which Bind
TITLE OF INVENTION: TO HIA Molecules, and the Use Thereof
TITLE OF INVENTION: TO HIA MOLECULES, and the Use Thereof
FILE REFERENCE: LUD 5483.2
CURRENT APPLICATION NUMBER: US/09/789,649
CURRENT APPLICATION NUMBER: US/09/099,543
PRIOR APPLICATION NUMBER: US 09/061,388
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-04-16
PRIOR FILING DATE: 1998-04-16
PRIOR FILING DATE: 1998-04-16
SROUR PRIOR FILING DATE: 1997-05-23
SRO ID NO 27
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: sequence located in CCKBR OR CCKRB at 310-319 and may intera OTHER INFORMATION: Sequence 3850 in this patent.
                           Sequence 3851, Application US/09572404B
Sequence 3851, Application US/09572404B
Sequence 3851, Correction No. US20030078374A1
SEMENAL INFORMATION:
APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome
FILE REPERBNGE: Human page: US/09/572,404B
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT PILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProtPatent version 1.0
SEQ ID NO 3851
LENGTH: 10
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Matches:
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                                                                                                                                                                                                                                                                                                                ORGANISM: Homo Sapiens
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Query Match:
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US-09-572-404B-3850
                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: sequence located in ATP5Al at 456-465 and may interact with Seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3850. Application US/09572404B
Publication No. US20030078374A1
SEQUENCE INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
COMPLETE OF INFORMATION: Complementary peptide ligands from the human genome FILE REFERENCE: Human patent
CURRENT PAPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SEQ ID NO 3850
LENGTH: 10
                                                                                                          Sequence 3688, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
   APPLICANT: Proteom Ltd
   TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT PILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: Protepatent version 1.0
; SOFTWARE: Protepatent version 1.0
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US-09-572-404B-3688
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1042 AGGCACCTGGTGGGGCC 1025
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                  4 ArgAlaProGlyGlyAla
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ORGANISM: Homo Sapiens
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Length:
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US-09-824-647-16 (1-2095) x US-10-216-122-80 (1-10)
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                                                                                                                                                                                                      1164 GGAGTGGGGCTGCTGTCC 1181
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Alignment Scores:
Pred. No.:
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                                                                                              RESULT 44

US-10-254-426-55

US-10-254-426-55

Sequence 55, Application US/10254426

Publication No. US20030113865A1

GENERAL INFORMATION:

APPLICANT: Busfield, Samantha J.

TILE OF INVENTION:

TILE REFRENCE: 07334-320001

CURRENT FILING DATE: 2002-09-25

PRIOR PRILING DATE: 2002-09-25

PRIOR APPLICATION NUMBER: US/09/731,449

PRIOR FILING DATE: 1999-09-09

PRIOR FILING DATE: 1999-09-03

PRIOR FILING DATE: 1998-09-30

NUMBER OF SEQ ID NOS: 62

NUMBER OF SEQ ID NOS: 62

LENGTHA: 10

ELENGTHE: 10

SEQ ID NO 55

LENGTH: 10
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APPLICANT: DeBerardinis, Ralph
TILL OF INVENTION: COMPOSITIONS AND METHODS OF USE OF MAMMALIAN RETROTRANSPOSONS
FILE REFERENCE: 053893-5006-03
CURRENT APPLICATION NUMBER: US/10/216,122
CURRENT FILING DATE: 2002-08-09
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Matches:
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Gaps:
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PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 1907-04-28
PRIOR FILING DATE: 1997-04-28
PRIOR APPLICATION NUMBER: US 08/749,805
PRIOR APPLICATION NUMBER: US 08/749,805
PRIOR PRIOR DATE: 1995-11-15
PRIOR FILING DATE: 1995-11-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 80, Application US/10216122 Publication No. US20030121063A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
; FEATURE:
OTHER INFORMATION: Fusion protein
US-10-254-426-55
                     903 GCAGCAGGTATAGCCATC 886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 CCCGGAGGAGCCAGCTAC 129
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SOFTWARE: Patentin version 3.1
SEQ ID NO 80
LENGTH: 10
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US-10-216-122-80
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7, 2003, 16:02:12 ; Search time 76.5 Seconds (without alignments) 5265.402 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                          protein search, using frame_plus_n2p model
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PH1639 PH1597 D35141

protein VP1 (EC 3.5.1.5

placental calcium-capsid protein VP1 urease (EC 3.5.1.5

Post-processing: Listing first 45 summaries

ALIGNMENTS		dextransucrase (EC 2.4.1.5) - Streptococcus bovis (fragment) C.Species: Streptococcus bovis	C:Jate: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 18-Sep-1996 C:Accession: PU0034	R;Uezono, Y.; Tsumori, H.; Mukasa, H. submitted to JIPID, October 1993	A:Description: Purification and properties of glucosyltransferase synthesizing 1 A:Reference number: PU0034	1: PU0034 type: protein	A; Residues: 1-11 <ue2></ue2>	A,Experimental source: ATCC 9809 C:Keywords: qlycosyltransferase; hexosyltransferase	interest		6.00 Matches: 6 nilarity: 100.00% Conservative: 0	Lty: 100.00%	1: 0.86% Indels: 0 2 Gaps: 0	US-09-824-647-16 (1-2095) x PU0034 (1-11)	1331 GAGACATCGGCTGTGACC 1348		2 GluThrSerAlaValThr 7		throward, mondo monacumant 1 t t t to the contract to
	RESULT 1 PU0034	dextransucr C.Species:	C; Date: 03-Feb-1994 C; Accession: PU0034	R; Uezono, Y submitted t	A:Reference	A; Accession: PU0034	A; Residues:	A; Experimen C; Keywords:	Altenment Scores	Pred. No.:	Score: Percent Similarity	Best Local Similarity	Query Match DB:	US-09-824-6	Oy 13		. q 0	RESULT 2	A29169
Command line parameters: -NODEL-frame+_n2p.model -DEV=xlp -O-/rmp 1/HighW groot/HG09894647/runa+ 07079003 154750 966954220 feats 1 9947	PS-7-31-7 OFFW-fastan -SUFFIX-11m.rpr -NIMATCH-0.1 -LOOPCL-0 -LOOPEXT-0 COUNTS-2-515 -START-1 -END1 -MATRIX-0ligo -TRANS-human40.cdi -LIST-45	DOCALIGN=200 "THE SCORE-quality "THE MIN"! ALIGN=45 "MODE=LOCAL "OUTFMT-pto NORM-ext "HEAPSIZE=500 "MINIEN"0 "MAXLEN"15	-USER-US09824647_@CGN_1_1_108_@runat_07072003_154759_26625 -NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG	-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7	PIR 73:*	1: pir1:* 2: pir2:*	3: pira:*	4: pir4:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed	and is derived by analysis of the total score distribution.	SUMMARIES	· ·	Query Score Match Length DB ID Description	11 2	6 0.9 12 2 A29169 phospholipase A2 (6 0.9 14 2 B60683 malate dehydrogena		5 0.7 8 2 A23967 leucopyrokinin - M 5 0.7 8 4 155411 hypothetical histo		5 0.7 9 2 A60957 thymocyte growth p
Command 111-MODEL-frag	-DB-PIR_73 -UNITS-bit	-NORM-ext	-USER-US091 -NO_MMAP -1	-DEV_TIMEO	Database :				Pred	and		,	Result No. So		0 0	ი 4	ບ	7	ω σ

dextransucrase (EC phospholipase A2 (malate dehydrogena H+-transporting tw leucopyrokinin - M	hypothetical histo thymic factor - pi thymocyte growth p xylose isomerase (macrophage cytotox calpain (EC 3.4.22 Achatina cardio-ex Ig H chain V-D-J r retinoic acid rece
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155411 A60957 A31576 **S39392**

A34662 PH1632 I54081

A60427

phospholipase A2 (EC 3.1.1.4) precursor - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Dacte: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 31-Oct-1997
C;Accession: A29169
C;Accession: A29169
Eur. J. Blochem. 53, 91-97, 1975

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C;Accession: 155411
R;Ivanova, V.S.; Hatch, C.L.; Bonner, W.M.
J; Biol. Chem. 269, 24189-24194, 1994
A;Title: Characterization of the human histone H2A.X gene. Comparison of its promot A;Reference number: 155411; MUID:95014156; PMID:7929075
                                                                                                                                                                                                                                                                                                                                                                                                                    R;Nachman, R.J.; Holman, G.M.; Cook, B.J.
Biochem. Biophys. Res. Commun. 137, 936-942, 1986
A;Title: Active fragments and analogs of the insect neuropeptide leucopyrokinin: st.
A;Reference number: A23967; WUID:86269041; PMID:3015140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:S73863; NID:9765295; PIDN:AAD14141.1; PID:94261841
A;Note: this is a hypothetical translation of a sequence from the promotor region F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C.Species: Homo sapiens (man)
C.Date: 28-Jan-2000 #sequence_revision 28-Jan-2000 #text_change 28-Jan-2000
                                                                                                                                                                                                                                                                                                                leucopyrokinin - Madeira cockroach
C;Species: Leucophaea maderae (Madeira cockroach)
C;Date: 31-Mar-1988 *sequence_revision 26-May-1994 #text_change 11-Jul-1997
C;Accession: A22967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein
A; Residues: 1-8 <NAC>
Kseywords: amidated cabboxyl end; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Leu) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Status: translation not shown; translated from GB/EMBL/DDBJ
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                                                                                     US-09-824-647-16 (1-2095) x S70719 (1-15)
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                                                                                                                                      US-09-824-647-16 (1-2095) x I55411
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Residues: 1-8 <IVA>
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## R: M. S. S. J. M. Y.; Szyroki, A.; Giles, I.G.; Moir, A.; O'Connor, C.D.

## Mol. Microbiol. 17, 523-531, 1995

## Reference number: S70719; MUID: 96100451; PMID: 8559071

## Reference number: S70719

## Reference number: S70719

## Residues: 1-15 CoIS-

## Residues: 1-15 CoI
  A; Title: Isolation and properties of prophospholipase A2 from ox and sheep pancreas. A; Reference number: A94661
A; Recession: A29169
A; Molecule type: protein
A; Residues: 1-12 < DUTY>
C; Superfamily: phospholipase A2
C; Reywords: carboxylic ester hydrolase; pyroglutamic acid
F; 1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                malate dehydrogenase (decarboxylating) (EC 1.1.1.39) - millet (fragment)
C;Species: Panicum sp. (millet)
R;Murata, T; Ikeda, J; Takano, M; Ohsugi, R.
Plant Cell Physiol. 30, 429-437, 1989
A;Title: Comparative studies of NAD-malic enzyme from leaves of various C-4 plants.
A;Reference number: A60683
A;Rocession: B60683
A;Rolcule type: protein
A;Residues: 1-14 <a href="Mainto-Millet">Millet</a>
C;Keywords: oxidoreductase; photosynthesis
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xylose isomerase (EC 5.3.1.5), intracellular - Streptomyces sp. (fragment) (Species: Streptomyces sp. (c)Species: Streptomyces sp. C. Date: 31-Mar-1990 % sequence_revision 31-Mar-1990 % text_change 28-Apr-1993 C; Accession: A31576 R; Pawar, H.S.; Kannan, K.; Srinivasan, M.C.; Vartak, H.G. Biochen, Blophys, Res. Commun. 155, 411-417, 1988 A; Title: Purification and characterisation of glucose (xylose) isomerase from Characterise chains sp. NCL 82-5-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   macrophage cytotoxicity-inducing factor, 29K - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: A66427
R;Jones, C.M.; Prince, C.A.; Williams, J.S.
Exp. Hematol. 19, 704-709, 1991
Exp. Hematol. 19, 704-709, 1991
A;Title: Purification and amino acid analysis of a human macrophage cytotoxicity-A;Reference number: A60427; MUID:91372335; PMID:1909970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Note: the sequence from the text on page 706 is inconsistent with that from pact; Reywords: cytokine
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C;Species: Sus scrofa domestica (domestic plg)
C;Species: Sus Scrofa domestica (domestic plg)
C;Species: Sus Scrofa domestica (domestic plg)
C;Species: S39392
R;Crawford, C.; Brown, N.R.; Willis, A.C.
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Mismatches:
Indels:
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A; Molecule type: protein
A; Residues: 1-9 - PRW>
C; Reywords: intramolecular oxidoreductase; isomerase
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   US-09-824-647-16 (1-2095) x A60957 (1-9)
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A; Residues: 'z',2-4,'z',6-9 <BAC>
C; Comment: This peptide induces DNA synthesis in immature thymocytes, but not peripheral
in a variety of immunoassays.
C; Comment: See PIR: A60957 (sheep) for discussion of another possible N-terminal modifica
C; Superfamily: thymic factor
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A.Molecule type: protein
A.Molecule type: Protein
A.Molecule type: PERN-
C.Comment: This peptide induces DNA synthesis in immature thymocytes, but not peripheral in a variety of immunoassays.
C.Comment: This peptide was isolated in two forms. One form contained the pyrrolidone car form (thymocyte growth peptide) contains a large, non-peptide blocking group with a hi
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C;Reywords: blocked amino end; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Glx) (in FTS) fstatus experimental
F;1/Modified site: blocked amino end (Glx) (in thymocyte growth peptide) fstatus experim
                                                                                                                                                                                                                                                                                                                        a peptide isolated from pig seru
                                                                                             N'Alternate names: FTS (facteur thymique serique)
C; Species: Sus scrofa domestica (domestic pig)
C; Species: 13.Jul-1981 $esquence_revision 13-Jul-1981 $text_change 07-May-1999
C; Accession: A01523; A60983
R; Pleau, J.M.; Dardenne, M.; Blouquit, Y.; Bach, J.F.
J; Biol. Chem. 252, 8045-8047, 1977
A; Title: Structural study of circulating thymic factor: a peptide isolated from A; Reference number: A01523; MuID:78026571; PMID:914862
A; Rocession: A01523
A; Molecule type: protein
A; Residues: 1-9 <PLE>
R; Bach, J.F.; Dardenne, M.; Pleau, J.M.; Rosa, J.
Nature 266, 55-57, 1977
A; Title: Blochemical characterisation of a serum thymic factor.
A; Reference number: A60983; MuID:77123829; PMID:300146
A; Accession: A60983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C:Reywords: pyrogiutamic acid
F:1/Wodified site: pyrrolidone carboxylic acid (Gln) #status experimental
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Matches:
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RESULT 7
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R; Dong, S.; Geng, J.P.; Tong, J.H.; Wu, Y.; Cai, J.R.; Sun, G.L.; Chen, S.R.; Wang, Genes Chromosomes Cancer 6, 133-139, 1993
A; Title: Breakpoint; Clusters of the PML gene in acute promyelocytic leukemia: priman A; Reference number: 154081; MUID:932222087; PMID:7682097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporo A; Reference number: PN0160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       malate dehydrogenase (EC 1.1.1.37) - fungus (Fusarium sporotrichioides) (fragment) C. Species: Fusarium sporotrichioides C. Species: Fusarium sporotrichioides C. Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 11-Nov-1994 C. Accession: PN0162 #sequence_revision 05-Aug-1994 #text_change 11-Nov-1994 #R. Fukaya, N.; Chow, L.P.; Sugiura, Y.; Tsugita, A.; Ueno, Y.; Tabuchi, K. submitted to JIPID, May 1994
                                                                                                                                                                                                                                                                       retinoic acid receptor alpha, exon 3 (mistranslated) - human (fragment) C;Species: Homo sapiens (man) C;Date: 04-Jun-1999 #sequence_revision 04-Jun-1999 #text_change 28-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:S57794; NID:g299073; PIDN:AAD13888.1; PID:g4261588 A;Note: the translation is from an incorrect reading frame
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Mismatches:
Indels:
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A;Map position: 17q12-17q12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1461 CGGCCAGCAGTGCTG 1447
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A;Molecule type: protein
A;Residues: 1-12 <FUK>
C;Keywords: oxidoreductase
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A; Residues: 1-11 <DON>
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R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
A;Title: Modecular characterization of transgene-induced immunodeficiency in B-less mice
A;Reference number: PH1580; MUID:93301609; PMID:8315387
A;Accession: PH1632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. J. 296, 135-142, 1993
A:Title: Studies of the active site of m-calpain and the interaction with calpastatin.
A:Reference number: S39391; WUID:94071815; PMID:8250833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PH1632
IG H chain V-D-J region (clone B-less 209) - mouse (fragment)
IG H chain V-D-J region (clone B-less 209) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-11 <ru>C;Reywords: amidated carboxyl end
C;Reywords: amidated carboxyl end (Phe) #status experimental
F;11/Modified site: amidated carboxyl end (Phe) #status
                                                                                                                                       calmodulin repeat homology hand; hydrolase
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A;Molecule type: protein
A;Residues: 1-11 <FUJ>
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A; Residues: 1-11 <LEV>
                                                                                 A; Status: preliminary
                                                              A; Accession: S39392
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R;Luo, S.; Martin, B.L.; Senshu, T.; Graves, D.J.
Arch. Biocohem. Biophys. 318, 362-369, 1995
A;Title: Enzymatic deimination of glyrocgen phosphorylase and a peptide of the phosphorence number: S65626; MUID:95251385; PMID:7733664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rigilmore, G.L.; Bard, J.A.; Birshtein, B.K.
J. Immunol. 141, 1754-1761, 1988
A;Title: DNA rearrangements affecting both variable and constant regions of Ig
A;Reference number: A30503; MUID:88315788; PMID:2842402
A;Accession: C30503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig gamma-2b chain C region (F5.5.1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 16-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Oryctolagus\cuniculus (domestic rabbit)
C;Date: 14-Feb.1997 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C;Accession: S65626
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A;Molecule type: protein
A;Residues: 1-3;4-12 <LUO>
                     A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-12 <WAL>
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A; Residues: 1-12 <GIL>
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  A; Accession: A60528
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R;Walton, P.E.; Baxter, R.C.; Burleigh, B.D.; Etherton, T.D.
Comp. Blochem. Physiol. B 92, 561-567, 1989
A;Title: Purification of the serum adid-stable insulin-like growth factor binding proteintherence number: A60528; MUID:89209787; PMID:2468442
                                                                                                                                                                        Ridinovilovic, M.; Mai, Y.; Herbstreith, M.; Rubboli, F.; Tarroni, P.; Clementi, F.; Ros Biochem. Biophys. Res. Commun. 197, 137-144, 1993
Biochem. Biophys. Res. Commun. 197, 137-144, 1993
Bicchem. Biophys. Res. Commun. 197, 137-144, 1993
A; Title: Splicing of an anti-sense Alu sequence generates a coding sequence variant for A; Reference number: 139390; MUID:94071933; PMID:8250918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T-cell receptor alpha chain V region (Cw3/Cas3) - human (fragment)
C;Species: Homo saplens (man)
C;Species: Homo saplens (man)
C;Species: Homo saplens (man)
C;Accession: PH1175
R;Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
A;Title: H.2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A;Reference number: S26512; MUID:92364546; PMID:1380061
                                                                                                                        C.Species: Homo sapiens (man)
C.Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        insulin-like growth factor-binding protein, serum - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 11-May-2000
                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:L18973; NID:g441143; PIDN:AAA86792.1; PID:g441144 C; Reywords: alternative splicing; neurotransmitter receptor
                                                                                                      cetylcholine receptor (alternative exon 5b) - human (fragment)
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Matches:
Conservative:
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Matches:
Conservative:
Mismatches:
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Best Local Similarity:
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A; Residues: 1-12 <RES>
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A; Holecule type: mRNA
A; Residues: 1-12 <CAS>
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C;Accession: PS0443
R;Adelman, J.P.; Shen, K.Z.; Kavanaugh, M.P.; Warren, R.A.; Wu, Y.N.; Lagrutta, A.; Neuron 9, 209-216, 1992
A;Title: Calcium-activated potassium channels expressed from cloned complementary I A;Reference number: JH0697; MUID:92360298; PMID:1497890
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C;Keywords: alternative splicing; ion channel; potassium channel; transmembrane pro
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C;Species: Gastroclonium coulteri
C;Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Drosophila melanogaster
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Feb-1997
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R;Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A;Title: Characterization of the bilin attachment sites in R-phycoerythrin. A;Reference number: A22565; MUID:85182601; PMID:3886644
A;Recession: G22565
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C;Comment: This potassium channel is activated by
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                                                                                                                      C; Keywords: neuropeptide; opioid peptide
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                                                  A; Molecule type: protein A; Residues: 1-13 <MIC>
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                         A; Status: preliminary
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A; Accession: A32734
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 30-Sep-1993
C;Accession: A33520
R;Blat, C.; Bohlen, P.; Villaudy, J.; Chatelain, G.; Golde, A.; Harel, L.
J;Blat, C.; Bohlen, P.; Villaudy, J.; Chatelain, G.; Golde, A.; Harel, L.
J;Blat, C.; Bohlen, P.; Villaudy, J.; Chatelain, G.; Golde, A.; Harel, L.
J;Flate: Isolation and amino-terminal sequence of a novel cellular growth inhibitor (inh A;Reference number: A33520; MUID:89197888; PMID:2703477
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enkephalin precursor - sheep (fragment)

c; Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

c; Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

c; Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

c; Species: Ovis orientalis aries, Ovis ammon 20-Jul-1990 *text_change 21-Jan-2000

c; Accession: A32734

k; Micanovic, R: Ray, P:; Kruggel, W.; Lewis, R.V.

Biochem: Biophys, Res. Commun. 118, 299-303, 1984

A; Title: Purification and sequence of an opioid peptide derived from ovine proenkephalin

A; Reference number: A32734; MUID:84128045; PMID:6546517
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R;Yorgey, P.; Lee, J.; Koerdel, J.; Vivas, E.; Warner, P.; Jebaratnam, D.; Kolter, R. Proc. Natl. Acad. Sci. U.S.A. 91, 4519-4523, 1994
A;Title: Posttranslational modifications in microcin B17 define an additional class of A;Reference number: A58375; MUD:94240167; PMID:8183941
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C;Species: Escherichia coli plasmid pPY113
C;Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 07-May-1999
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                           CGGACTTCTCCACGT 427
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A;Wolecule type: protein
A;Residues: 1-12 <YOR>
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A;Molecule type: protein
A;Residues: 1-12 <BLA>
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C;Accession: A01777
R;Hirai, Y.; Yasuhara, T.; Yoshida; H.; Nakajima, T.
Bibmed. Res. 2, 447-449, 1981
A;Hitle: A new mast cell degranulating peptide, mastoparan-M, in the venom of the A;Reference number: A01777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: B61233

R; Thatcher, M.J.D.; Shille, V.M.; Fliss, M.F.; Bazer, F.W.; Sisum, W.; Randal, Biol. Reprod. 44, 108-120, 1991

A; Title: Characterization of feline conceptus proteins during pregnancy. A; Reference number: A61233; MUID: 91198359; PMID: 2015342

A; Accession: B61233
         conceptus protein 4 - cat (fragment)
C;Species: Felis silvestris catus (domestic cat)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conceptus protein 4 - cat (fragment)
C;Species: Felis silvestris catus (domestic cat)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
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C;Species: Vespa mandarinia
C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 08-Dec-1995
                                                                           R;Thatcher, M.J.D.; Shille, V.M.; Fliss, M.F.; Bazer, F.W.; Sisum, W.; F
Biol. Reprod. 44, 108-120, 1991
A;Title: Characterization of feline conceptus proteins during pregnancy.
A;Reference number: A61233; MUID:91198359; PMID:2015342
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Conservative:
Mismatches:
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C; Keywords: amidated carboxyl end; venom
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A; Molecule type: protein
A; Residues: 1-13 <THA>
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A;Molecule type: protein
A;Residues: 1-13 <THA>
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Best Local Similarity:
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                                                             C; Accession: B61233
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                                                                                                                                                                                                                                                                                               Score:
                                                                                                                                                                                                                                                 C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 16-Aug-1996
C; Accession: B61458
R; Brouet, J.C.; Dellaqi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.
J. Exp. Med. 170, 1551-1558, 1989
A; Title: Expression of a public idiotype by human monoclonal IgM directed to myelin-assc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T-cell antigen receptor VJ junction beta chain - human C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999 C; Accession: $47388 R; Lehner, P.J. submitted to the EMBL Data Library, August 1994 A; Reference number: $47355 A; Reference number: $47355 A; Recession: $47388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:235710; NID:9527515; PIDN:CAA84779.1; PID:9527516
C;Keywords: T-cell receptor
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Matches:
Conservative:
Mismatches:
Indels:
       Mismatches:
Indels:
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                                             Gaps:
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A;Molecule type: protein
A;Residues: 1-13 <BRO.
C;Keywords: heterotetramer; immunoglobulin
                                                                               (1-13)
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A;Molecule type: mRNA
A;Residues: 1-13 <LEH>
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C;Accession: PH1767
R;POCTCALLI, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A;Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: $57574
R;Burrows, S.R.; Silins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argaet, V.P.
submitted to the EMBL Data Library, June 1995
A;Description: T cell receptor repertoire for a viral epitope in humans is diversif
A;Reference number: $57494
                                                                                         C;Accession: PH1763
R;Porcelli, S.;Yrockey, C.E.; Brenner, M.B.; Balk, S.P.
R;Porcelli, S.;Yrockey, C.E.;
A;Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cell receptor alpha chain V region (clone 2V alpha 7.2-2) - human (fragment)
                             receptor alpha chain V region (clone 1V alpha 23-2) - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
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C;Species: Homo sapiens (man)
C;Date: 19-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999
                                                        C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
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A; Accession: PH1763
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-14 < POR>
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A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-14 < POR>
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Query Match:
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A;Molecule type: mRNA
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C; Date: 13-3nn-1995 #sequence_revision 13-Jan-1995 #text_change 29-May-1998
C; Accession: S23376
R; Gaill, F.; Wiedemann, H.; Mann, K.; Kuehn, K.; Timpl, R.; Engel, J.
J. Mol. Biol. 221, 209-223, 1991
A; Title: Molecular characterization of cuticle and interstitial collagens from worms A; Reference number: S17581; MUID:92015209; PMID:1920405
A; Recession: S23376
A; Reseaton: S23376
A; Residues: 1-14 cGAI>
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Plant Cell Physiol. 30, 429-437, 1989
A;Title: Comparative studies of NAD-malic enzyme from leaves of various C-4 plants.
                                                                                                                                                                                                                                                                                                                                                                                C;Species: Panicum sp. (millet)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 24-Feb-1994
C;Accession: B60683
                                                                                                                                                                                                                                                                                                                                                         malate dehydrogenase (decarboxylating) (EC 1.1.1.39) - millet (fragment)
F;14/Modified site: amidated carboxyl end (Leu) #status experimental
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A;Residues: 1-14 <MUR>
C;Reywords: oxidoreductase; photosynthesis
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A; Accession: B60683
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Rickinson, D. M.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A; Ettle: Molecular characterization of transgene-induced immunodeficiency in B-le
A; Reference number: PH1580; MUID:93301609; PMID:8315387
A; Accession: PH1639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RiLevinson, D.A.; Campos-Torres, J.; Leder, P.
L. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-16
A;Reference number: PH1580; MUID:93301609; PMID:8315387
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C;Species: Mus musculus (house mouse)
31-Aug-1990 #sequence_revision 31-Aug-1990 #text_change 30-May-1997
C;Accession: D35141
R;Sim, G.K.; Augustin, A.
Cell 61, 397-405, 1990
A;Title: Dominantly inherited expression of BID, an invariant undiversified T cel
A;Reference number: A35141; MUID:90242386; PMID:2110506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1597
                                                                                                   Ig H chain V-D-J region (clone B-less 230) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun.1994 #sequence_revision 02-Jun.1994 #text_change@17-Mar-1999
C;Accession: PH1639
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A; Residues: 1.14 <LEV>
A; Experimental source: bone marrow pre-B lymphocyte
C; Keywords: immunoglobulin
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                                                             RESULT 38
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R; Coleman, M.E.; Pan, Y.C.E.; Etherton, T.D.
Biochem. Biophys. Res. Commun. 181, 1131-1136, 1991
A;Title: Identification and NH2-terminal amino acid sequence of three insulin-like growth; Reference number: JH0515; MUID: 92109718; PMID: 1722398
A; Accession: JH0516
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R; Coleman, M.E.; Pan, Y.C.E.; Etherton, T.D.
Biochem. Biophys. Res. Commun. 181, 1131-1136, 1991
A; Title: Identification and NH2-terminal amino acid sequence of three insulin-like growt A; Reference number: JH0515; MUID:92109718; PMID:1722398
A; Accession: JH0516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Insulin-like growth factor-binding protein 3 - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 23-Mar-1995
                                                                                                                                                                                                                                                                                                                                                                                                      nsulin-like growth factor-binding protein 3 - pig (fragment)
Species: Sus scrofa domestica (domestic pig)
Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 23-Mar-1995
                   A;Cross-references: EMBL:Z49959; NID:g887504; PIDN:CAA90230.1; PID:g887505
C;Keywords: T-cell receptor
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A; Residues: 1-14 <COL>
A; Experimental source: serum
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A;Residues: 1-14 <COL>
A;Experimental source: serum
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267 GGGCAGCAACTGGA 253

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C.Accession: PQ0545
R.Davison, M.D.; Rixon, F.J.; Davison, A.J.
J. Gen. Virol. 73, 2709-2713, 1992
A.Stitle: Identification of genes encoding two capsid proteins (VP24 and VP26) of he A;Reference number: PQ0544; MUID:93019027; PMID:1328483
                                                                                                                                                                                                                                                                                                                                                        K;KO, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau Mamm. Genome 5, 349;355, 1994
A;Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
A;Reference number: 148934; MUID:94319082; PMID:8043949
A;Recession: 149407
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C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
                                                                                                                                                                                                                                                                              placental calcium-binding protein - western wild mouse (fragment)
C;Species: Mus spretus (western wild mouse)
C;Date: 02-Jul.1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999
C;Accession: 14407
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C;Superfamily: S-100 protein; calmodulin repeat homology
C;Reywords: calcium binding; EF hand
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A; Residues: 1-15 <RES>
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Rytakabashi, T.; Moyer, M.P.; Cano, M.; Wang, Q.J.; Mountjoy, C.P.; Sanger, W.; Adrian, Carcinogenesis 16, 931-939, 1995

A;Title: Differences in molecular biological, biological and growth characteristics betw A;Reference number: 152734; MUID:95246257; PMID:7728976

A;Reference number: 152734; MUID:95246257; PMID:7728976

A;Reference number: 152734

A;Reference number: 152734

A;Reference number: 152734

A;Reference number: 152734

A;Reference: GB/EMBL/DDBJ

A;Residues: 1-15 < CRES

A;Residues: 1-15 < CRES

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A;Residues: 1-15 < CRES

C;Genetics: A;Residues: GB:S77068; NID:9914176

C;Genetics: A;Residues: CA;Residues: CA;Reywords: GPP binding
                                                                                                                                                                                                                                                                                                                                                                                                                                        leader peptide - Thermus aquaticus
C;Species: Thermus aquaticus
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999
C;Accession: 500901
R;Croft, J.E.; Love, D.R.; Bergquist, P.L.
Mol. Gen. Genet. 210, 490-497, 1987
A;Title: Expression of leucine genes from an extremely thermophilic bacterium in Escheri
A;Reference number: 500901; MUID:88121725; PMID:3323845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene c-K1-ras protein - hamster (fragment)
C;Species: Cricetinae gen. sp. (hamster)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 28-May-1999
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A; Residues: 1-15 <CRO>
A; Cross-references: EMBL:X06604; NID:g48244; PIDN:CAA29823.1; PID:g48245
A; Note: the source is designated as Thermus thermophilus
C; Superfamily: Thermus aquaticus leu leader peptide
                         not compared with conceptual translation
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    A; Accession: D35141
A; Status: preliminary; not c
A; Molecule type: mRNA
A; Residues: 1-14 <SIN>
C; Keywords: T-cell receptor
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-I MISCELLANDROUS: AN ANALOG WITHOUT THE N-TERMINAL PCA RESIDUE WAS SYNTHESIZED AND FOUND TO EXHIBIT GREATER ACTIVITY (144%) THAN THE PARENT NEUROPEPTIDE. THE PORTION OF THE SEQUENCE OF LAR MOST CRITICAL FOR THE MYOTROPIC PROPERTIES IS LIMITED TO THE PENAMENT PRACTICE ENAMENT FIPRI.

-I SIMILARITY: BELONGS TO THE PYROKININ FAMILY.

PIR; A23967; A23967.
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01-FBB-1994 (Rel. 28, Last sequence update)
01-FBB-1994 (Rel. 28, Last annotation update)
10-FBB-1994 (Rel. 28, Last annotation update)
Leukopyrokinin (LPK) (LEM-PK).
Leucophaea maderae (Madeira cockroach).
Eukaryota: Merazoa: Arthropoda: Mandibulata; Pancrustacea; Hexapoda;
Insecta: Pterygota: Neoptera: Orthopteroidea; Dictyoptera; Blattaria;
Blaberoidea; Blaberidae: Leucophaea
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MEDLINE=8105251; PubMed-2877794;

Holman G.W., Cook B.J., Nachman R.J.;

Primary structure and synthesis of a blocked myotropic
neuropeptide isolated from the cockroach, Leucophaea maderae.*;

Comp. Biochem. Physiol. 95:219-224(1986).

- FONCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
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P16339
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Nachman R.J., Holman G.M., Cook B.J.;
Active fragments and analogs of the insect neuropeptide leucopyrokinin: structure-function studies.";
Biochem. Biophys. Res. Commun. 137:936-942(1986).
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ODP2_BOVIN
PNEU_HUMAN
                RS7_MYCIT
UF06_MOUSE
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UPAA_HUMAN
VGLG_HSV2B
AL11_CARMA
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SAP_STOVA
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PROSITE; PS00539; PYROKININ; 1.
Neuropeptide; Amidation; Pyrokinin.
MOD_RES 8 8 AMIDATI
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vespa manda
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physcomitre
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litoria gil
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morganella
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(without alignments)
5891.045 Million cell updates/sec
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P19149
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Compugen Ltd.
                                                                                   protein search, using frame_plus_n2p model
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                                                                                                                                                                                                                                                                                                                                                               112892 seqs, 41476328 residues
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                GenCore version
Copyright (c) 1993 - 2003
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LPL_THETH
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CDN2_LITGI
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XYLA_STRSQ
CEP1_ACHFU
CD14_LITXA
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Match Length
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Maximum DB seq length: 15
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Conservative: Mismatches: Indels:

Length: Matches:

9.22e+06 5.00

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Isomerase; Pentose shunt; Xylose metabolism; Magnesium
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                                                                                                                                                                              INTERPITO: IPRO01998; Xylose isom.
PROSITE; PS00172; XYLOSE_ISOMERASE_1; PARTIAL.
PROSITE; PS00173; XYLOSE_ISOMERASE_2; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09:824-647-16 (1-2095) x XYLA_STRSQ (1-9)
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100.00%
0.73%
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Best Local Similarity:
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    Pawar H.S., Kannan K., Srinivasan M.C., Vartak H.G.; Perification and characterisation of glucose (xylose) isomerase from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces. NCBL_TaxID=1931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pleau J.-M., Dardenne M., Blouquit Y., Bach J.-F.; Structural study of circulating thymic factor: a peptide isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thymic factor.
Sus scrofa (P1g).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from pig serum. II. Amino acid sequence.";
from pig serum. II. Amino acid sequence.";
-1- MISCELLANEOUS: THE BIOLOGICAL SOURCE(S) AND PHYSIOLOGICAL
ACTIVITIES OF THIS PEPTIDE HAVE NOT BEEN DETERMINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 PYRROLIDONE CARBOXYLIC ACID.
MW; D500B87866C5B33D CRC64;
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        949 MW; 92341771A9D5A1B6 CRC64;
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Mismatches:
Indels:
                                                                 Length:
Matches:
Conservative:
Mismatches:
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01-NOV-1990 (Rel. 16, Last sequence update)
11-NOV-2002 (Rel. 41, Last annotation update)
Xylose isomerase (EC 5.3.1.5) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 AA.
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Matches:
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                                                                                                                                                                                                           US-09-824-647-16 (1-2095) x LPK_LEUMA (1-8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces sp. (strain NCL 82-5-1).
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                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-78026571; PubMed-914862;
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                                                                 1.04e+07
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Best Local Similarity:
                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
DB:
          AA;
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P19149;
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          SEQUENCE
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cardio-excitatory peptide-1 (ACEP-1).
Achatina fulica (Giant African snail).
Bukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
Achatinacea; Achatinidae; Achatina.
                                                                                                                                                                                                                                                                                                                                                                   AMIDATION.
82D6D5B9C7741365 CRC64;
                                                                                                                                                                                                                                                                                                                     MOVEMENT OF ACHATINA.
-!- SIMILARITY: TO POSSIBLE PEPTIDE L5 FROM APLYSIA
                                                                                                                                                                                                                                                                                                                                                                                                                  0000
                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                         11 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps:
                                                                                                                                                                                                        STRAIN-Ferussac; TISSUE-Heart atrium;
                                                                                   01-AUG-1991 (Rel. 19, Created)
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5.00
100.00%
100.00%
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AA; 1305 MW;
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3 AlaGlySerAlaHis 7
                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                           PIR; A34662; A34662.
                                                                                                                                                                                                                                                                                                                                                      Hormone; Amidation.
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secretions of rainbow trout, Oncorhynchus mykiss.";
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                                                                                                                                                                                                                                                                                                                           RESULT 7
                                                                                                                                                                                          Pred.
MEDLINE-97374000; PubMed-9230483;
Steinborner S.T., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Skin mucus;
Fernandes J.M.O., Kemp G.D., Molle G., Smith V.J.;
"Antimicrobial properties of a histone H2A-like protein from skin
                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoldea; Hylidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
NCBI_TaxiD-8022;
                                                                                                                                                                                                         "New caerin antibacterial peptides from the skin glands of the Australian tree frog Litoria xanthomera."; J. Pept. Sci. 3:181-185(1997).
                                                                                                                                                                                                                                                                                                                                                     -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS
                                                                                                                                                                                                                                                                                                                                                                                   AMIDATION.
28225503E3772728 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                            0000
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Matches:
Conservative:
Mismatches:
Indels:
                                             15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                      Litoria xanthomera (Orange-thighed frog), and Litoria chloris (Blue-thighed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                            12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 AA.
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                             PRT;
                                                                                                                                                          SEQUENCE, AND MASS SPECTROMETRY.
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                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 12 AA; 1097 MW;
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5.00
100.00%
100.00%
0.72%
                                                                                                                                                                                                                                                                                                                                                                         Amphibian skin; Amidation.
MOD_RES 12 12
                            STANDARD;
                                                                                                                                      MCBI_TaxID-79697, 86064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                            Pelodryadinae; Litoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Histone H2A (Fragment)
Oncorhynchus mykiss (R
                                                                                                                                                                     SPECIES-L. xanthomera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                            Caeridin 1.4
                                                                                                                                                                                                  Ramsay S.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H2AX_ONCMY
                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                            CD14_LITXA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
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MEDLINE-21605839; PubMed-11738233;
Maillo M., Aguilar M.B., Lopez-Vera E., Craig A.G., Bulaj G.,
Olivera B.M., Reimer de la Cotera E.P.;
"Conorfamide, a Conus venom peptide belonging to the RFamide family of neuropeptides.";
H2A, H2B, H3, and H4; which wrap approximately 146 bp of DNA-

-- SUBCELLULAR LOCATION: Nuclear.
-- HASS SPECTROMETRY: MW=13639; METHOD-MALDI.
-- SIMILARITY: BELONGS TO THE HISTONE H2A FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- SUBCELLULAR LOCATION: Secreted.
-i- TISSUE SPECIFICLITY. Expressed by the venom duct.
-i- MASS SPECTROMERIX: MM-1454.8; METHOD-ELECTROSPIRY.
-i- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conus spurius (Alphabet cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=192919;
                                                                      InterPro; IPR002119; Histone H2A.
PROSITE; PS00046; HISTONE H2A; PARTIAL.
Chromosomal protein; Nucleosome core; Nuclear protein;
DNA binding; Antibiotic; Fungicide; Acetylation.
NON_TER
                                                                                                                                                                                                               3EF28D9668D87DD8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 12 AMIDATION.
AA; 1456 MW; 2510671E49D772D3 CRC64;
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                                                                                                                                                                                                                                                                            0000
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                Conservative:
                                                                                                                                                                                                                                                                                                                                    Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Conorfamide-Srl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1- FUNCTION: Causes hyperactivity in mice.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
                                                                                                                                                                                                                                                                          Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY
                                                                                                                                                                                                                                                                                                                                                      Indels:
                                                                                                                                                                             ACETYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-824-647-16 (1-2095) x H2AX_ONCMY (1-12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1391 AGGGTGGGAGCTGGG 1405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neurotoxin; Toxin; Amidation.
                                                                                                                                                                                               12
1202 MW;
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5.00
100.00%
0.73%
                                                                                                                                                                                                                                                                        5.8e+04
5.00
                                                                                                                                                                                                                                                                                                            100.008
100.008
0.728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 ArgValGlyAlaGly 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Toxicon 40:401-407(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                    Best Local Similarity:
                                                                                                                                                                                                                 12 AA;
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                Percent Similarity
                                                                                                                                                                                                                                                       Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RF1_CONSP
P58805;
                                                                                                                                                                         MOD_RES
NON_TER
SEQUENCE
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Percent Similarity:
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             Alignment Scores:
Pred. No.:
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                                                                                                                                                                                                                                                                      CDN3_LITGI
P56248;
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P82077;
                                                                                                                                                                                                                                                                                                                                                        Caeridin 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                          Query Match:
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                                                                                                                                                                                                                                                          CDN3_LITGI
                                                                                                                                                                                                                                        RESULT 10
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                                                                                                                                                                                                          Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
Aculeata; Vespoidea; Vespidae; Vespinae; Vespa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Parotoid gland;
Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.;
Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.;
Peptides from Mustralian frogs. The structures of the caerins and
caeridins from Litoria gilleni.";
J. Chem. Res. 139:937-961(1993).
-1- FUNCTION: CAERLINES SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Litoria gilleni (Centralian tree frog).

Litoria gilleni (Centralian tree frog).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;

Pelodryadinae; Litoria.

NCBI_TaxID=39405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMIDATION.
06F1BBF272550CBF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 AA; 1480 MW; C85A7ECA1D7B00DD CRC64;
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Mismatches:
Indels:
                                                                                                                        20-MAR-1987 (Rel. 04, Created)
20-MAR-1987 (Rel. 04, Last sequence update)
01-MUC-1992 (Rel. 23, Last annotation update)
MASTCDATAN M (Mast cell-degranulating peptide).
Vespa mandarinia (Hornet).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                               14 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (1-14)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMIDATION.
                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-824-647-16 (1-2095) x MAST_VESMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE, AND MASS SPECTROMETRY.
555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               571 CTGGCAAAGAAGCTC 585
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5.00
100.00%
100.00%
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                            œ
           GlyTrpValProVal
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GGGTGGGTGCCCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                               STANDARD;
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity
                                                                                                                                                                                                                                                                                                             rissue-venom;
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P56247;
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                                                                                               MAST_VESMA
P04205;
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SEQUENÇE
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569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOD_RES
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                                                                            MAST_VESMA
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                                                             RESULT
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ANTIBIOTIC ACTIVITY.
-I- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
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Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.;
Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.;
Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.;
Caeridins from Litoria gilleni.";
J. Chem. Res. 139:937-961(1993).
-i- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Litoria caerulea (Green tree frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
Pelodryadinae; Litoria
                                                                                                                                                                                                                                                                                                                                                                                                                                     Litoria gilleni (Centralian tree frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
Pelodryadinae; Litoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMIDATION.
06E90A797AF70CBF CRC64;
  15
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Mismatches:
Indels:
                                       Conservative:
Mismatches:
Indels:
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30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                         [-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                    15 AA
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Matches:
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  Length:
Matches:
                                                                                                                                               US-09-824-647-16 (1-2095) x CDN2_LITGI (1-15)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-824-647-16 (1-2095) x CDN3_LITGI (1-15)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE, AND MASS SPECTROMETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             915 GGGGCCTGGGGCTG 929
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5.00
100.00%
100.00%
0.72%
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5.57e+04
5.00
100.00%
100.00%
0.72%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 AA; 1430 MW;
                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                      STANDARD;
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Best Local Similarity:
Query Match:
                                                                 Best Local Similarity:
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15 AA.

PRT;

STANDARD;

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LPL_THETH P21234;
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SEQUENCE
                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LPL_THETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
  J. Chem. Soc. Perkin Trans. 1:573-576(1993).
-1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC ACTIVITY.
-1- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL.
         Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.; "Peptides from Australian frogs. Structures of the caeridins from
                                                                                                                                                                                                                                                                                                                                                                                                                                           Conus betulinus (Beech cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=89764;
                                                                                                                                                                                                                                                                                                                                                                                                                           Chen J.-S., Fan C.-X., Hu K.-P., Wei K.-H., Zhong M.-N.; "Studies on conotoxins of Conus betulinus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROBABLE.
PROBABLE.
3749B4F08E311337 CRC64;
                                                                                                               9FF1A646BD550CAE. CRC64;
                                                                                                                                            0000
                                                                                                                                                             Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                          15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                         15 AA.
                                                                                                                                           Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
                                                                                  -1- MASS SPECTROMETRY: MW-1355; METHOD-FAB
Amphibian skin; Amidation.
MOD_RES 15 15 AMIDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (1-15)
                                                                                                                                                                                                             US-09-824-647-16 (1-2095) x CDN5_LITCE (1-15)
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                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-20058566; PubMed-10591037;
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                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE, AND MASS SPECTROMETRY.
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5.00
100.00$
100.00$
0.72$
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                                                                                                              SEQUENCE 15 AA; 1357 MW;
                                                                                                                                                                                                                                         11 GlyGlyLeuGlyLeu 15
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                                                                                                                                           5.57e+04
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100.00%
100.00%
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                                                                                                                                                                                0.72%
                                                                                                                                                                                                                                                                                         STANDARD;
TISSUE-Parotoid gland;
                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
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                            Litoria caerulea.
                                                                                                                                                                                                                                                                                                                                         Conotoxin BeTXIb.
                                                                                                                                 Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Venom
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                                                                          GLANDS.
                                                                                                                                                                                                                                                                                         CX1B_CONBE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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CX1B_CONBE
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RESULT 13 DIDH_PSESP

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This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                 Oppermann U.C.T., Maser E.;
"Characterization of a 3 alpha-hydroxysteroid dehydrogenase/carbonyl "Characterization of a 3 alpha-hydroxysteroid dehydrogenase/carbonyl reductase from the Gram-negative bacterium Comamonas testosteron1.";
Eur. J. Biochem. 241:744-749(1996).

-1- FUNCTION: ALONG WITH THE 3 ALPHA-HYDROXYSTEROID DEHYDROGENASE AND 3-0XO-REDUCTASE ACTIVITIES TOWARDS A VARIETY OF CIS OR TRANS FUSED A/B RING STEROIDS, IT ALSO REDUCES SEVERAL XENOBIOTIC CARBONYL COMPOUNDS) INCLUDING A METYRAPONE-BASED CLASS OF INSECTICIDES, TO
                                                                                                                                                                                                                                                                                                                                                                                                            THE RESPECTIVE ALCOHOL METABOLITES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Croft J.E., Love D.R., Bergquist P.L.; Expression of leucine genes from an extremely thermophilic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gen. Genet. 210:490-497(1987).
FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    3,17-dione + NAD(P)H.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                    01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
3-alpha-hydroxysteroid dehydrogenase (EC 1.1.1.50) (3-alpha-HSD)
(Hydroxyprostaglandin dehydrogenase) (HSD29) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Thermus/Deinococcus group; Deinococci; Thermales; Thermaceae; Thermus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INVOLVED IN COFACTOR BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9506860D070A7790 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15
5
0
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Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 18, Last sequence update)
(Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SDK) FAMILI.
InterPro; IPR002198; ADH_Short.
PROSITE; PS00061; ADH_SHORT; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-HB8 / ATCC 27634;
MEDLINE-88121725; PubMed-3323845;
                                                                                                                                                                                                               MEDLINE-97100200; PubMed-8944761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequ
30-MAY-2000 (Rel. 39, Last anno
(Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1193 GCCTCTGGGATTGGA 1179
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1315 MW;
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5.00
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100.00%
0.73%
                                                                                                                           Bacteria, Proteobacteria.
NCBL_TaxID=306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thermus thermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00061; AL
Oxidoreductase; NAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15
15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leu leader peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SDR) FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OF LEUCINE.
                                                                                                       Pseudomonas sp
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01-OCT-1996
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score:
                            (See http://www.isb-sib.ch/announce/
                                               and for commercial
Swiss Institute of Bioinformatics and the EMBL outstation
               There are no restrictions on ng as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plastid enzymes.

1 CATALYTIC ACTIVITY: ATP + 3-phospho-D-glycerate = ADP + 3-phospho-D-glyceraty; ATP + 3-phospho-D-glycerate = ADP + 3-phospho-D-glyceraty; ATP + 3-phospho-D-glyceraty; Calvin cycle.

1 SUBUNIT: MONOMER (BY SIMILARITY).

1 SIMILARITY: BELONGS TO THE PHOSPHOGLYCERATE KINASE FAMILY.

1 THEAPPO, IPROGLIST; PGLYCERATE KINASE; PARTIAL.

PROSITE; PSO0111; PGLYCERATE KINASE; PARTIAL.

Transferase; Kinase; Multigene family; Calvin cycle; Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 34, Last sequence update)
Phosphoglycerate kinase, chloroplast (BC 2.7.2.3) (Fragment).
Physcomitrella patens (Moss).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Punarildae; Funariales; Funariaceae; Physcomitrella.
                                               Usage by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1531 MW; 56A5ECC1F677EEC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      00002
                                                                                                                                            tide; Leucine biosynthesis.
15 AA; 1666 MW; C2F107A386D7620B CRC64;
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Conservative:
Mismatches:
                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
             the European Bioinformatics Institute. There use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (see hor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                                                           Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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MEDLINE-97275459; PubMed-9129336;
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5.00
100.00%
100.00%
0.72%
                                                                                                               EMBL; X06604; CAA29823.1; -.
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100.00%
100.00%
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                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
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                                                                                                                                              Leader peptide;
SEQUENCE 15 A
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   the
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Р80659;
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Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
Pernollet J.-C., Zivy M., de Vienne D.,
"The maize two dimensional gel protein database: towards an integrated
genome analysis program.";
                                                                                                                      Zea mays (Maize).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyma; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                              Theor. Appl. Genet. 93:997-1005(1896).
-i- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 4.9, ITS MW IS: 31.6 kDa.
Maize-2DPAGE: P80631; COLEOPTILE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=90564298; PubMed=2345135;
MEDLINE=90564298; PubMed=2345135;
MEDLINE=90564298; PubMed=2345135;
Morganella morganii urease: purification, characterization, and isolation of gene sequences. 7
J. Bacteriol. 172:3073-3080(1990).
-I- CAPALTIC ACTIVIT: Urea + H(2)0 - CO(2) + 2 NH(3).
-I- SIMILARIT: ACTIVIT: UREASES BETA SUBUNITS.
-I- SIMILARITY: TO OTHER UREASES BETA SUBUNITS.
-I- SIMILARITY: TO OTHER UREASES BETA SUBUNITS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Morganella morganii (Proteus morganii).
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                   01-OCT-1996 (Rel. 34, Created)
1-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Unknown protein from 2D-page of etiolated coleoptile (Spot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1990 (Rel. 15, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Urease beta subunit (EC 3.5.1.5) (15 kDa subunit) (Urea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 15 15 15 15 AA; 2D98944F2F20C7E8 CRC64;
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NON_TER 15 15
SEQUENCE 15 AA; 1580 MW; 83C54CFOCE1614D0 CRC64;
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Matches:
Conservative:
Mismatches:
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15 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1861 GGAGGCCTGAGCAGA 1847
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5.00
100.00%
100.00%
0.73%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amidohydrolase) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
STANDARD;
                                                                                                                                                                                                                                                              TISSUE-Coleoptile;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                    MaizeDB; 123957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Morganella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             URE2_MORMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase.
 UC25_MAIZE
                                                                                                              (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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Alignment Scores

ThrGluGlnAlaSer 7

RESULT 16

919 MW; 8D3DC40B19CDC2D2 CRC64;

84000

Conservative: Mismatches: Indels:

100.00% 100.00% 0.58%

Gaps:

Length: Matches:

1.04e+07 4.00

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ubmitted (DEC-1997) to the SWISS-PROT data bank.

1- CAUTION: We are unable to find this protein in the translation of the genome of strain H37Rv.
                                                                                                                                                                                                                                                                                                   US-09-824-647-16 (1-2095) x NS3_MYCTU (1-8)
                                                                                                                                                                                                                                                                                                                                         815 GTGGTAGCGTTC 804
                                                                                                                                                                                                                                                                                                                                                                1 ValvalAlaPhe 4
                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                   8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1767;
                                                                                                                                          Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
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ID RS7_MYCIT
AC P33564;
        Submitted
                                                                                 NON_TER
SEQUENCE
                                                                 NON_TER
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Query Match:
                                                                                                                                                                                                                                            Query Match:
                                                                                                                                                                Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RPSG.
                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 20
                                                                                                                                                                                       Score:
        500FF68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A novel D-leucine-containing Conus peptide: diverse conformational
                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda; Neogastropoda; Conoidea; Conldae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 D-LEUCINE.
890 MW; 75A367672732CEB8 CRC64;
  Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative:
Mismatches:
Indels:
                                                             Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
30 kba non-secretory protein 3 (Fragment)
                                                                                                                                                                                                                                                                                                                                     15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                   8 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYNTHESIS, AND MASS SPECTROMETRY.
                                                                                                                                          (1-15)
                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-Clipperton Island; TISSUE-Venom; MEDLINE-99388839; PubMed-10461743;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-824-647-16 (1-2095) x COW2_CONPU (1-8)
                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                      US-09-824-647-16 (1-2095) x URE2_MORMO
                                                                                                                                                                                                                                                                                                                                                                                                                   Conus purpurascens (Purple cone).
                                                                                                                                                                             1827 ACCCCACTCGGAGGG 1841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.04e+07
4.00
100.00%
100.00%
0.58%
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Prasad H.K., Annapurna P.S.;
    .57e+04
.00
                                                                                                                                                                                                 ThrProLeuGlyGly 11
                                  100.00%
100.00%
0.72%
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                              Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                  Leu-contryphan-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-41690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Olivera B.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                   CONPU
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P81152;
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9
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    Pred.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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(See http://www.isb-s1b.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium intracellulare.*;
Nucleic Acids Res. 21:1039-1039(1993).
-!- FUNCTION: PROFIEIN S7 BINDS SPECIFICALLY TO PART OF THE 3' END OF
16S RIBOSOWAL RNA (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE S7P FAMILY OF RIBOSOWAL PROFEINS.
                                                                                                                                                                                      Mycobacterium intracellulare.
Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                            Nair J., Rouse D.A., Morris S.L.; "Nucleotide sequence analysis of the ribosomal S12 gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0000
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Conservative:
Mismatches:
Indels:
                                                                                Last sequence update)
Last annotation update)
8 AA.
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Interpro; IPR000235; Ribosomal_S7; PARTIAL.
Ribosomal protein; rRNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (or send an email to license@lsb-slb.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-824-647-16 (1-2095) x RS7_MYCIT (1-8)
                                                                                                                                    30S ribosomal protein S7 (Fragment)
  PRT;
                                                                                                                                                                                                                                                                                                                                                   MEDLINE-93197130; PubMed-8451173;
                                                 01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequ
01-FEB-1994 (Rel. 28, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L08171; AAA25376.1; -.
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  STANDARD;
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Best Local Similarity:
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NON_TER 8
SEQUENCE 8 AA;
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UF06_MOUSE

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Liljeqvist J.-A., Svennerholm B., Bergstrom T.;
Submitted (APR-1999) to the SWISS-PROT data bank
-!- MISCELLANDOUS: HENER ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AND
2: GH, GB, GC, GG, GI, AND GE.
-!- MISCELLANEOUS: GLYCOPROTEIN G IS WUCH LARGER IN HSV-2 THAN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Plasma protein map: an update by microsequencing.";
Electrophoresis 13:707-714(1992).
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 7, ITS MIS: 12 kDa.
SWISS-2DPAGE; P30096; HUMAN.
                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                      01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Unknown protein from 2D-page of plasma (Spot 36) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                      PEDDINE-33092937; PubMed-1459097;
Hughes G.J., Futtiger S., Paquet N., Ravier F., Pasquall C.
Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
Hochstrasser D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycoprotein G (Fragment).

Herpes simplex virus (type 2 / strain B4327UR).
Viruses; GsDMA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86677B59D1A72042 CRC64;
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Matches:
Conservative:
Mismatches:
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15-JUL-1999 (Rel. 38, Last annotation update)
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Gaps:
                               US-09-824-647-16 (1-2095) x UF06_MOUSE (1-8)
                                                                                                                                                                                      PRT;
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15-JUL-1999 (Rel. 38, Last sequ
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                                                                                                                                                                                  UPAA_HUMAN , STANDARD;
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P81780;
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SEQUENCE
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-I- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI'OF THIS UNKNOWN NOW-TER 15:2, ITS MW IS: 50 kba.
                                                                                                                                                                                                                                                                                                                                      MEDLINE-95009907; PubMed-7523108;
Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
Mersick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
Separation and sequencing of familiar and novel murine proteins
using preparative two-dimensional gel electrophoresis.";
Electrophoresis 15:335-445(1994).
-I- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 5.2, ITS MW IS: 50 kDa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-007-1994 (Rel. 30, Created)
01-007-1994 (Rel. 30, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
Unknown protein from 2D-page of fibroblasts (P50) (Fragment).
Wins musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; MuscBL_TaxID=10090;
                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                           01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
Unknown protein from 2D-page of fibroblasts (P50) (Fragment).
Mus musculus (Mouse).
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Conservative:
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                                                                                            PRT;
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                                                                                            STANDARD;
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TISSUE-Fibroblast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score:
Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
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Aliqument Scores:

Pred.

Query Match:

SEQUENCE

SEQUENCE

UF06_MOUSE

RESULT 22

Alignment Scores:

Pred. No.:

Query Match;

SEQUENCE

SEQUENCE

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MEDLINE-88058932; Pubmed-3680228;
Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,
Gray W.R., Olivera B.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-stomach;
MEDLINE-92082847; PubMed-1747388;
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4.00
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                                                                                                                                                                                                                                                       Hormone; Amidation.
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Query Match:
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                                                                                                                                                                                                                                                                                          9 AA;
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                                                                                        REVIEW
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                                                                                                                                                                                                                                                                                                                                               Score:
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                                                                                                                                                                                                                                                                                                                  Carcinus maenas (Common shore crab) (Green crab).
Eukaryota, Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
Brachyura; Eubrachyura; Portunoidea; Portunidae; Carcinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       IISSUE=Cerebral ganglion, and Thoracic ganglion;
MEDLINE=98121193; PubMed=9461295;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conus striatus (Striated cone).
Sukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=6493;
           683 MW; 7847686772C865B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 AA; 927 MW; 832D79CDCB46D861 CRC64;
                                                 Length:
Matches:
Conservative:
Mismatches:
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Conservative:
Mismatches:
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1988 (Rel. 09, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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                                                                                                                                       US-09-824-647-16 (1-2095) x VGLG_HSV2B (1-8)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMIDATION
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01-NOV-1988 (Rel. 09, Last seq
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4.00
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100.00%
0.58%
                                                1.04e+07
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100.00%
100.00%
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                                                                                                                                                                1834 AGTGGGGTCCCG 1823
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                                                                                                                                                                             2 SerGlyValPro 5
                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity:
Query Match:
                                                                                      Best Local Similarity:
                                                                                                                                                                                                                                                                                                     Carcinustatin 11.
             8 AA;
                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=6759;
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                                                                         Percent Similarity
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                                      Alignment Scores:
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P05487;
                                                                                                                                                                                                                                         AL11_CARMA
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NON_TER
SEQUENCE
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                                                                                                  Query Match:
                                                                                                                                                                                                                                                   P81814;
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                                                 Pred. No.:
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                                                                                                                                                                                                                  RESULT 25
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Lunalyola; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea; Nephropoidea; Nephropoidae; Nephrops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Favrel P., Kegel G., Sedlmeier D., Keller R., van Wormhoudt A.; *Structure and biological activity of crustacean gastrointestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptides identified with antibodies to gastrin/cholecystokinin.";
"Invertebrate vasopressin/oxytocin homologs. Characterization of peptides from Conus geographus and Conus straitus venoms."; J. Biol. Chem. 262:15821-15824(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY PIR; A48398; A48398.
                                                                                                          Biochimie 73:1233-1239(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                        9 AMIDATION.
1031 MW; 17EB176EB4540050 CRC64;
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Mismatches:
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Mismatches:
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01-MAR-1992 (Rel. 21, Last sequence update)
01-MAR-1992 (Rel. 21, Last annotation update)
03-MAR-1992 (Rel. 21, Last annotation update)
03-MAR-1992 (Rel. 21, Last annotation update)
Nephrops norvegicus (Norway lobster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 AA.
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Matches:
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                                                                                                                                                                                                                                                                                                                                     Pfam; PF00220; hormone4; 1.
PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
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"Eight novel FMRFamide-like neuropeptides isolated from the nematode
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Best Local Similarity:
                                                                                                                                                                     Best Local Similarity:
Query Match:
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                                                                                                                                                            Percent Similarity:
                Ascaris suum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
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OXYF_SCYCA
ID OXYF_SCYCA
                                                                                                                       Alignment Scores:
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P42996;
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MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                       Asvatocin.
                                                      FAMILY
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                                                                                                                                                                                                                                                                                                          RESULT 30
                                                                                                                                    pred.
     S FE CCR FF
                                                                                                                                                                                                                                                                                       TISSUB-Suboesophageal ganglion, and Thoracic ganglion;
MEDLINE-88077077; PubMed-3689410;
Proux J.P., Miller C.A., Li J.P., Carney R.L., Girardie A.,
Delaage M., Schooley D.A.;
Identification of an arginine vasopressin-like diuretic hormone from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
Ascarididae; Ascaris.
                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
Acridomorpha; Acridoidea; Acrididae; Oedipodinae; Locusta.
                                                                                                                                                                                                                                                                                                                                                                                                      1- SUBUNIT: F2 IS AN ANTIPARALLEL DISULFIDE LINKED DIMER OF F1.
1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERCHAIN (WITH C-6') (IN F2). INTERCHAIN (WITH C-1') (IN F2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56EB176EB451A057 CRC64;
                                                                                                                                                                                                                                                                                                                                                                             Biochem. Biophys. Res. Commun. 149:180-186(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
                                                                                                                                                 01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
10-DEC-1998 (Rel. 37, Last annotation update)
Locupressin (Diuretic neuropeptide F1/F2).
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                                                                                                                        9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (1-9)
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                 US-09-824-647-16 (1-2095) x D1_NEPNO (1-9)
                                                                                                                                                                                                      locust)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IN F1.
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                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95380362; PubMed=7651904; Cowden Ç., Stretton A.O.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neuropeptide; Amidation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FMRFamide-like neuropeptide AF9
                                                                                                                                                                                                       Locusta migratoria (Migratory
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0.58%
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                                           1955 TCAGAAGGGGGT 1966
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                                                                                                                         STANDARD;
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                          NCBI_TaxID=7004;
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                                                                                                                        DNF1_LOCMI P16339;
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P43172;
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SEQUENCE
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                                                                                                             DNF1_LOCMI
                                                                                                 RESULT 28
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Scyllorhinus canicula (Spotted dogfish) (Spotted catshark).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
Scyllorhinidae; Scyllorhinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Pituitary;

MEDLINE-95062247; PubMed=7972045;

Chauvet J., Roullle Y., Chauveau C., Chauvet M.-T., Acher R.;

Chauvet J., Roullle Y., Chauveau C., Chauvet M.-T., Acher R.;

"Special evolution of neurohypophysial hormones in cartilaginous
fishes: asvatocin and phasvatocin, two oxytocin-like peptides
fishes: asvatocin and phasvatocin, two oxytocin-like peptides
fisolated from the spotted dogfish (Scyllorhinus caniculus).";

Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).

-1- FUNCTION: DISPLARS OXYTOCIC ACTIVITY ON RAT UTENUS.
-1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
                       THE FARP (FMRFAMIDE RELATED PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   640000
                                                                                       AMIDATION.
524F073774176877 CRC64;
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17EDD76EB444404B CRC64;
                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
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PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
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                                                                                                                                                                                                                                                                                              Gaps:
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Interpro; IPR001230; Prenyl_site.
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4.00
100.00%
100.00%
0.58%
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4.00
100.00%
100.00%
0.58%
Peptides 16:491-500(1995).
-i-.SIMILARITY: BELONGS TO
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                                                                                                            9 AA; 1012 MW;
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                                                                                                                                                                                                                                                                                                                                                                                   283 CCACGGCCTCTG 272
                                                              Neuropeptide; Amidation.
MOD_RES 9 9
SEQUENCE 9 AA; 1012 MW
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Endocrinol, 70:152-157(1988).

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US-09-824-647-16 (1-2095) x OXYV_SQUAC (1-9)
                        :1 - FUNCTION: ANTIDIURETIC HORMONE
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  TOUR BEEFES
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Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
Characterization of neurohypophyseal hormones from a fresh water bony fish, the carp (Cyprinus carplo). Comparison with hormones from sea water bony fishs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Petromyzon marinus (Sea lamprey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                            Scyllorhinus canicula (Spotted dogfish) (Spotted catshark).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Blasmobranchi; Galeomorphil; Galeoidea; Carcharhiniformes;
Scyllorhinidae; Scyllorhinus.
NCBI_FaxID=7830;
                                                                                                                                                                                                                                                                                                                 Chauvet J., Roulle Y., Chauveau C., Chauvet M.-T., Acher R.,
"Special evolution of neurohypophysial hormones in cartilaginous
fishes: asvatocin and phasvatocin, two oxytoch-like peptides
isolated from the spotted dogfish (Scyliorhinus caniculus).";
Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
-I- FOWATION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTERUS.
-I- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY:
InterPro: IPRO00981; Neurhyp_horm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17EDD76EB44449DB CRC64;
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Matches:
Conservative:
Mismatches:
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01-NOV-1991 (Rel. 20, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00220; hormone4; I.
PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-824-647-16 (1-2095) x OXYF_SCYCA (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMIDATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and
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                                                                                                                                                                                                                                                                           TISSUE-Pituitary;
MEDLINE-95062247; PubMed-7972045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cyprinus carpio (Common carp),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      683 TGCCCAGTGGGA 694
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NCBI_TaxID=7962, 7757;
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Best Local Similarity:
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                                                                                             Phasvatocin.
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P23879;
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DB:
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OXYT_CYPCA
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MEDLINE-73031727; PubMed-5083097;
Acher N. Chauvet J., Chauvet M.-T.;
"Phylogeny of the neurohypophysial hormones. Two new active peptides isolated from a cartilaginous fish, Squalus acanthias.";
Eur. J. Blochem. 29:12-19(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE.
MEDLINE-72128038; PubMed-4622083;
Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
"Identification of 2 new neurohypophyseal hormones, valitocin (Val8-"Identification of 2 new neurohypophyseal hormon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Squalus acanthias (Spiny dogfish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Squalea; Squaloidei; Squalidae; Squalus.
NCBI_TaxID-7797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, spiny dog-fish (Squalus acanthias).";
C. R. Acad. Sci., D, Sci. Nat. 274:313-316(1972).
-1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY. InterPro; IPR000981; Neurhyp_horm.
InterPro; IPR001230; Prenyl_site.
                                                                                                                                                                                36.
-i - SIMITARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY. PIR; B61364; B61364. B61365; S06375; S06375.
                                                                                                                                                                                                                                                                                                                   9 AMIDATION.
1053 MW; 17EB176EB456D04B CRC64;
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Conservative:
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Conservative:
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Valitocin.
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                                                                                                                                                           Pfam; PF00220; hormone4; 1. PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
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DISULFID 1
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P43000;
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MOD_RES
SEQUENCE
                                                                                                                              InterPro;
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Percent Similarity
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Hypothetical
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P30426;
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ID BRK_O
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                                                                                                                                                                                                                                                                                                                                                                                                    Stomopneutes variolaris (Sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Diadematacea; Phymosomatoida; Stomechinidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disulfide linkage-containing sperm-activating peptide by tandem mass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                spectrometry.";
FEBS Lett. 224:179-182(1991).
-!- FUNCTION: CAUGES STIMULATION OF SPERM RESPIRATION AND MOTILITY
THROUGH INTRACELLURAR ALKALINIZATION, TRANSIENT ELEVATIONS OF
CAMP, CGMP AND CLACIUM LEVELS IN SPERM CELLS, AND TRANSIENT
ACTIVATION AND SUBSEQUENT INACTIVATION OF THE MEMBRANE FORM OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Egg jelly;
MEDLINE-92097763; PubMed=1756858;
Yoshimo K.-I., Takao T., Shimonishi Y., Suzuki N.;
"Determination of the amino acid sequence of an intramolecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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"Unification of the ferritin family of proteins.";
Proc. Natl. Acad. Sci. U.S.A. 89:2419-2423(1992).
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9 AA; 1010 MW; C469B3387B076EB9 CRC64;
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01-MAY-1992 (Rel. 22, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein in BFR 3'region (Fragment).
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Last annotation update)
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MEDLINE-92196129; PubMed-1549605;
                                                                                                                                                                                                                                                               01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last seq
01-MAR-1992 (Rel. 21, Last ann
                                                                                                                                                                                                                                                                                                                                                                            Sperm-activating peptide (SAP)
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683 TGCCCAGTGGGA 694
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                                                                                                                                                                                                STANDARD;
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S19329; S19329.
                                   CysProValGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-7663;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stomopneustes
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                                                                                                                                                                                                       SAP_STOVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match:
DB:
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                                                                                                                                 RESULT
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cintra A.C.O., Vieira C.A., Giglio J.R.;

Cintra A.C.O., Vieira C.A., Giglio J.R.;

"Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.";

J. Protein Chem. 9:21-227 (1990).

-1- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE ANGOTERNIA-CONVERTING FURNEME AND ENHANCES THE ACTION OF BRADXKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.

IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Queimada jararaca).
Lepidosauria; Squamata; Chordata; Craniata; Vertebrata; Euteleostomi;
Viperidae; Crotalinae; Bothrops.
1111-TaxID-8723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
Bradykinin-potentiating peptide 55,1 (Angiotensin-converting
enzyme inhibitor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PYRROLIDONE CARBOXYLIC ACID. 2FF835545761F6D8 CRC64;
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                                                                                                                                                                              DF98B5A1B417776D CRC64;
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Matches:
Conservative:
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Matches:
institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                 US-09-824-647-16 (1-2095) x YBFR_AZOVI (1-9)
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MEDLINE-90351557; PubMed-2386615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1993 (Rel. 25, Created)
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4.00
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4.00
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100.00%
0.58%
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100.00%
0.58%
                                                                                                                                                                              947 MW;
                                                                                                EMBL; M83692; AAA22122.1;
PIR; B41983; B41983.
                                                                                                                                                                                                                                                                                                                                                                                                                      Hypotensive agent; Venom.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    464 GGGCAGCACCCC 453
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Best Local Similarity:
                                                                                                                                                                                  AA;
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-- TISSUE SPECIFICITY: GNRH NEDRONS LIE WITHIN BLOOD SINUSES CLOSE TO THE GONODUCTS AND GONADS IN BOTH JUVENILES AND ADULTS, IMPLYING THAT THE NEUROPPETIDE IS RELEASED INTO THE BLOODSTREAM.
-- MASS SPECTROMETRY: MM-1117.52; METHOD-MALDI.
                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-96413669; PubMed-8816823;
Powell J.F.F., Reska-Skinner S.M., Prakash M.O., Fischer W.H.,
Park M., Rivier J.E., Crang A.G., Mackie G.O., Sherwood N.M.;
"Two new forms of gonadotropin-releasing hormone in a protochordate
                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Corellidae; Chelyosoma.
NCBL_TaxID=71177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rana ridibunda (Laughing frog) (Marsh frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBI_TaxID=8406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and the evolutionary implications.";
Proc. Natl. Acad. Sci. U.S.A. 93:10461-10464(1996).
-1- FUNDON: STEMULATES THE SECRETION OF BOTH LUTEINIZING AND
FOLLICLE-STIMULATING HORMONES.
                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Gonadoliberin II (Gonadotropin-releasing hormone II) (GnRH-II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMIDATION (BY SIMILARITY).
284B38D1EEB735A3 CRC64;
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Matches:
Conservative:
Mismatches:
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01-NOV-1991 (Rel. 20, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 AA.
                                                                                                                              10 AA.
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MEDLINE-91315477; PubMed-1859413;
Conlon J.M., O'Harte F., Vaudry H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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4.00
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100.00%
0.58%
1416 CTGGCAGCAGGC 1405
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                                                                                                                                STANDARD;
                                            4
                       1 LeuAlaAlaGly
                                                                                                                                                                                                                                                                     (Luliberin: II).
Chelyosoma productum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 AA;
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Best Local Similarity:
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                                                                                                             GON2_CHEPR
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                                                                                      RESULT 39
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                                                                                                                                  16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
15-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MISSING (IN 2ND COMPONENT).
/FTId-VAR_005255.
CFEEC6AB02C3387D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bradykinin; Vasodilator.
SEQUENCE 10 AA; 1193 MW; 33C59075A3786777 CRC64;
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Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
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Matches:
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MEDLINE~75150968; PubMed~5538385;
                                                                                                                                                                                                                                                                   MEDLINE-94039817; PubMed-8224232;
                         Created)
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Query Match:
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P01358:
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Query Match

GAJU_HUMAN RESULT 38

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01-JUL-1989 (Rel. 11, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Dihydrollpoamide acetyltransferase component of pyruvate dehydrogenase
complex (EC 2.3.1.12) (E2) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Component J. 245:919-922(1987).

-I FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall conversion of pyruvate to acetyl-CoA and CO(2). It contains multiple copies of three enzymatic components: pyruvate dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and lipoamide dehydrogenase (E3).

-I CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA + S-acetyldihydrolipoamide.

-I COFACTOR: THE E2 COMPONENT CONTAINS TWO COVALENTLY-BOUND LIPOYL
"Primary structures of the bombesin-like neuropeptides in frog brain show that bombesin is not the amphibian gastrin-releasing peptide."; Biochem. Biochem. Biochem. Biochem. Biochem. Biochem. Biochem. Biochem. EdgesLudlak LOCATION: Secreted.
-: SUBCELLULAR LOCATION: Secreted.
-: SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: FORMS A 24-POLYPEPTIDE STRUCTURAL CORE WITH OCTAHEDRAL SYMMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus (Bovine).
Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-88024154; PubMed-3117054;
Bradford A.P., Howell S., Aitken A., James L.A., Yeaman S.J.;
Bridford Y.P., Howell S., Aitken A., James L.A., Yeaman S.J.;
Bridford T. Stroken S.J.;
Sprangonent of bovine heart pyruvate dehydrogenase complex.";
Blochem. J. 245:919-922(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycolysis; Transferase; Acyltransferase; Repeat; Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BELONGS TO THE 2-OXOACID DEHYDROGENASE FAMILY CONTAINS 2 LIPOYL-BINDING DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    889BECD1ADD33AB1 CRC64;
                                                                                                                                                                                                                                                                                      AMIDATION. F81FBAE862CDC371 CRC64;
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003016; L1poyl.
PROSITE; PS00189; LIPOYL; PARTIAL.
                                                                                                                                                     PIR; PQ0177; PQ0177.
InterPro; IPR000874; Bombesin.
Pfam; PF02044; Bombesin; 1.
PROSITE; PS00257; BOMBESIN; 1.
BOmbosin family; Amidation.
MOD_RES 10 10 AM
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4.00
100.00%
100.00%
0.58%
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P11180;
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TISSUE-Lung;
MEDLINE-91110910; PubMed-2274681;
Batta V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;
Batta V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;
Pneumadin: a new lung peptide which triggers antidiuresis.";
Regul. Pept. 30:77-87(1990).
-!- FUNCTION: AWTIDIURETIC PEPTIDE THAT TRIGGERS THE RELEASE OF ADH.
PIR; B33143; B33143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Batra V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;
"Ineumadin: a new lung peptide which triggers antidiuresis.";
Regul. Pept. 30,77-87(1990).
-i- FUNCTION: THIS ANTIDIURETIC PEPTIDE TRIGGERS THE RELEASE OF ADH.
                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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640378DAA723276B CRC64;
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Conservative:
Mismatches:
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Mismatches:
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16-OCT-2001 (Rel. 40, Last annotation update)
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16-OCT-2001 (Rel. 40, Last annotation update)
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                                   Matches:
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SEQUENCE 10 AA; 956 MW;
                5.45e+05
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                                                                                                                                                                                                                                                           STANDARD;
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Rattus norvegicus (Rat).
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Homo sapiens (Humah)
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                                              Percent Similarity:
Best Local Similarity
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Alignment Scores:
Pred. No.:
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P22103;
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MOD_RES
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                                                                                Query Match:
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us-09-824-647-16.lim.rsp

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7 AsnGlnIleLeu 10
                                                                                 P56923;
30-MAY-2000
                                                                   FEMK_RANTE
                                                                                                                                     remporin K,
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                                                                                                                                                                                                                                                                               Barra D.;
                                                                                                                                                                                                                       SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                 01-JUN-1994 (Rel. 29, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
18-MA polymerase beta subunit (EC 2.7.7.48) (Large structural protein)
(L protein) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION IN MRNA SYNTHESIS, CAPPING, METHYLATION AND POLY(A) SYNTHESIS OF WEAR SYNTHESIS OF OFFILE FOR STRINGS, RNA EDITING OF THE GENE TRANSCRIPT, PROTEIN KINNSE ACTIVITY:
-1- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Ulster/88;
BLDILKE-29268877;
PubMed=1588321;
Curran M.D., O'Loan D., Kennedy S., Rima B.K.;
"Molecular characterization of phocine distemper virus: gene order and sequence of the gene encoding the attachment (H) protein.";
J. Gen. Virol. 73:1189-1194(1992).
-i- FUNCTION: PROBABLE COMPONENT OF THE ACTIVE POLYMERASE. IT MAY
                                                                                                                                                                                                                                                                                                                                                                                                    Phocine distemper virus (PDV).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Morbillivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        {RNA}(N).
-i- SIMILARITY: WITH L PROTEIN OF OTHER PARAMYXOVIRUSES.
                           AMIDATION.
641D00DAA723276B CRC64;
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Matches:
Conservative:
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Matches:
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Indels:
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Transferase; RNA-directed RNA polymerase.
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P35946;
01-JUN-1994 (Rel. 29, Created)
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10 AA; 1048 MW;
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PIR; A33143; A33143.
Amidation.
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                                                                   Alignment Scores:
                                        SEQUENCE
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-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
                                                                                                                                                                                                                                                                                                         "Temporins, antimicrobial peptides from the European red frog Rana temporaria.";
                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana
                                                                                                                                                                                                                                                                                                                                                         Eur. J. Biochem. 242:788-792(1996).
                                                                                                                                                                                                                                                                            Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
                                     it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amphibian skin; Antibiotic; Amidation; Multigene family. MOD RES 10 10 AMIDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AMIDATION.
390549B337272457 CRC64;
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Conservative:
Mismatches:
Indels:
                                   30-MAY 2000 (Rel. 39, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
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                                                                                                                   Rana temporaria (European common frog).
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PRT;
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MEDLINE-97175050; PubMed-9022710;
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STANDARD;
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Job time: 33.5 secs
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Best Local Similarity:
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060614 homo sapten
091938 homo sapten
051997 homo sapten
065901 leavenworth
054226 saccharopol
013695 homo sapten
013695 homo sapten
090c37 homo sapten
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lupinus lut
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Q9e1t8 hepatitis
252840 rhizobium l
                                                         rattus sp.
bradypodion
                                                                                                                                 calumma nas
                                                                                      calumma boe
                                                                                                    calumma fur
                            bos taurus
bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                hepatitis
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Q9elu1 hepatitis
Q9elu0 hepatitis
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STRAIN-NC16-2, TC29-5, AND TC97;
TTRANSPSSON-FNS641A1, TNS641B1, AND TNS641D1;
Kholodii G.Y., Gorlenko Z.M., Mindlin S.Z., Nikiforov V.G.;
Bistribution of distinct microvariants of Tn5641 in environmental bacteria.";
                                                                                                                                                                                                                                                                                                                     Q93x21 2
Q93wf2 1
Q69232 P
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09elu4 |
.09elu3 |
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01-JUN-2002 (TrEMBLrel, 21, Last annotation update)
Porin-like protein (Fragment).
Pseudomonas fluorescens.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                           P82923 b
09tru6 b
09t2p3 r
08shp0 b
08shm2 c
08shm3 c
08sh13 c
                                                                                                                                           098905
070580
090346
090347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AJ422128; CAD19527.1; -. EMBL; AJ422129; CAD19528.1; -. EMBL; AJ422130; CAD19529.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 AA; 1206 MW; 23C47E7401F5A417 CRC64;
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Q9EIU6
Q9EIU5-
Q9EIU4-
Q9EIU3
Q9EIU1
Q9EIU1
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Q9E1T8
Q52840
008979
P83056
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Q91XP1
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Q13695
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NCBI_TaxID=294;
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Q8RJF1
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-QP-QDA2_1/YOPPO_SOO_1/YOSQB24647/runat_07072003_154759_26619/app_query.fasta_1.2247
-QP-QDA2_1/YOSPO_SOO_1/YOSQB24647/runat_07072003_154759_26619/app_query.fasta_1.2247
-QDS-SPREMBL_21 -QEWT=fastan -SUFFIX=1im.rspt -WINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=0.11go -TRANS=human40.cdi
-LIST=45 -DGALIGN=200 -THR_SCOREM=QUA11ty -THR_MIN=1 -ALIGN=45 -WODE=LOCAL
-USER-T-pto -NORM-ext -HEAPSIZE=500 -WINICEN=0 -WAXLEN=15
-USER-USO9824647_CGGN_1 1_231_erunat_07072003_154759_26619 -NCPU=6 -ICPU=3
-NO_WMAP -LAGREQUERY -NEC_SCORES=0 -WAIT -DSPBLOCK=100 -LONGIGG
-FGAPOP=60 -YGAPOP=60 -YGAPEXT=60 -DELGD=6 -DELGRET=7
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6466.947 Million cell updates/sec
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 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

    protein search, using frame_plus_n2p model

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                                                                                                                                                                                                                                                                                           671580 seqs, 206047115 residues
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sp_human:*
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Maximum DB seq length: 15
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us-09-824-647-16.lim.rspt

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J. Virol. 71:5080-5087(1997).
EMBL; Y11802; CAA72496.1; -.
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Best Local Similarity:
Query Match:
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Best Local Similarity:
                                                             9 AA;
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*Organization and Unusual Expression of Histone Genes in the Sea Star Pisaster ochraceus.*;

J. MOI. Evol. 25:29-36(1987).

BEMBL; X05619; CAA29106.1;

NON_TER. 11 11
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-NURI: TISSUE-MURINE RETROVIRUS INDUCED TUMOR;
STRAIN-NURI: TISSUE-MURINE RETROVIRUS INDUCED TUMOR;
STRAIN-NURI: DEPENDED 188573;
Amtoft H.W., Sorensen A.B., Bareil C., Schmidt J.; Luz A., Pedersen F.S.;
Pedersen F.S.;
"Stability of AML1 (core) site enhancer mutations in T-lymphomas induced by attenuațed SL3-3 murine leukemia virus mutants.";
                                                                                                                                                                                                                                                                                                                                                                   Pisaster ochraceus (Sea star).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa; Asteroidea; Forcipulatacea; Forcipulatida; Asteriidae; Pisaster.NCBI_TaxID=7612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER 11 11 SEQUENCE 11 AA; 1128 MW; 5173974A3865BDD3 CRC64;
                                   0000
                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Sea StAR histone H2B gene 5'region (Fragment).
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Last annotation update)
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Matches:
Conservative:
Mismatches:
Indels:
                               Length:
Matches:
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Mismatches:
Indels:
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Best Local Similarity:
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                                                               Percent Similarity:
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ACCOCCOS NA REPAREMENTAL STATEMENT OF STATEM

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TISSUE-SKIN SECRETION;
Chen T. B., OTT D.F., Bjourson A.J., McClean S., Rao P.F., Shaw C.;
"Cloning and post-translational processing of frog skin kininogens.";
submitted (JUL-2001) to the SWISS-PROT data bank.
-1 - SUBCELLULIAR LOCATION: SECRETED.
-1 - TISSUE SPECIFICITY: SKIN.
SEQUENCE 9 AA: 1048 MW; 3393D771A9C87DC7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
Bradykinin-like peptide ([Ala3,Thr6]bradykinin).
Bombina variegata (Tellow-bellied toad).
Bukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE.
TISSUE-LIVER;
Roc E.C., Burkhart W., Blackburn K., Moseley A., Spremulli L.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Mitochondrial 28S ribosomal protein S2 (MRP-S2) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
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981 MW; 293E01E865A776D8 CRC64;
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Matches:
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Conservative:
Mismatches:
Indels:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10118;
  01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Cytochrome P-450 27/25-HYDROXYLASE-52 kDa isoform (Fragment).
                                                                                                     SEQUENCE.
MEDIINE-91355184; PubMed-1883820;
Addya S., Zheng Y.M., Shayiq R.M., Fan J.Y., Avadhani N.G.;
"Characterization of a female-specific hepatic mitochondrial
cytochrome:P-450 whose steady-state level is modulated by
testosteroñe.";
                                                                                                                                                                                                      10 10
10 AA; 1092 MW; 316CEFB4072DDDC7 CRC64;
                                                                                                                                                                          Biochemistry 30:8323-8330(1991).
                                                                                                                                                                                                                                                                                Percent Similarity:
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                                       Mitochondrion.
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SEQUENCE
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                                                                                                                                                                                                                                                                        Score:
   "Small subunit of the mammalian mitochondrial ribosome. Identification of the full complement ribosomal proteins present.";
Submitted (DEC-2000) to the SWISS-PROT data bank.
-1 - SUBCELIGIAR LOCATION: MITOCHONDRIAL.
-1 - SIMILARITY: BELONGS TO THE S2P FAMILY OF RIBOSOMAL PROTEINS.
InterPro; IPR001865; Ribosomal_S2.
                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEWBLrel. 13, Created)
01-MAY-2000 (TrEWBLrel. 13, Last sequence update)
01-WAY-2000 (TrEWBLrel. 21, Last sequence update)
01-WON-2002 (TrEWBLrel. 21, Last annotation update)
GAP-3, GTPase-activating protein (Fragment).
Bos taurus (Bovine).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
NCBL_TaxID-9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The purification of a Rapl GTPase-activating protein from bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-92112868; PubMed-1309786;
Nice E.C., Fabri L., Hammacher A., Holden J., Simpson R.J.,
Burgess A.W.;
                                                                                                                                                       10 AA; 1246 MW; 6A7A6679C04B476B CRC64;
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                                                                 Pfam; PF001316; Ribosomal_S2, PRTIAL. PRINTS; PR00395; RIBOSOMALS2; PRRTIAL. PROSTRE: PS00962; RIBOSOWAL_S2_1; PARTIAL. Ribosomal protein; Mitochondrion.
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J. Biol. Chem. 267:1546-1553(1992).
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Townsend T.M., Larson A.L.; "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the Chamaeleonidae (Reptilia, Squamata)."; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF448727; AAL90463.1;
                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae;
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01-JUN-2002 (TrEMBLrel. 21, Last seq
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Mitochondrion.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria: Squamata; Iguania; Acrodonta; Chamaeleonidae; Calumma.
NCBI_TaxID=179902;
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Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Calumma
NCBI_TaxID=179899;
                                                                                                                                                                                                                                                                                                                                              Townsend T.M., Larson A.L.;
"Molecular Phylogenetics and Mitochondrial Genomic Evolution in the "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the Chamaeleonidae (Epetlila, Squamata).";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF448733; AAL90481.1;
MAItochondrian.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Calumma.
NCBI_TaxID=179905;
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"Molecular Phylogenetics and Mitochondrial Genomic Evolution in the Chamaeleonidae (Reptilia, Squamata).";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR440740; AAL90502.1;
Mitochondrion.
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"Molecular Phylogehetics and Mitochondrial Genomic Evolution in the Chammaleonidae (Reptilla, Squamata).";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF4448737; AAL90493.1;
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Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Calumma.
NCBL_raxID=179903;
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01-JUN-2002
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Viruses; SERNA positive-strand viruses, no DNA stage; Flaviviridae; GBV-C/HGV group.
NCBI_TaxID=45255;
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GBV-C/HGV group.
NCBL_TaxID=45255;
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HFGV isolates from Singapore: Evidence for novel Asian variants.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF078058; AAC32365.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wong S.B.J., Chan S.H., Ren E.C.;
"Diversity of GB virus C/hepatitis G virus isolates in Singapore:
predominance of group 2a and the Asian group 3 variant.";
J. Med. Virol. 58:145-153(1999).
EMBL; ARO78055; AAC32362.1;
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MEDLINE-99266893; Pubmed-10335862;
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Hepatitis G virus.
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Sowden J., Smith H., Morrison K., Edwards Y.;
Sowden J., Smith H., Morrison K., Edwards Y.;
Sewden J., Smith H., Morrison K., Edwards Of the proximal promoter of the carbonic anhydrase 3 (CA3) gene.";
Gene 214:157-165(1999).
EMBL; AJ006474; CANO7057.1;
MGD; MGI:1311477; Cars.
                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
S3 peptide (Fragment).
Glycine max (Soybean).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudlcotyledons; core eudlcots; Rosidae;
eurosids I; Fabales; Fabaceae; Papillionoideae; Phaseoleae; Glycine.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
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01-AUG-1998 (TrEMBLrel. 07, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
Carbonic anhydrase III (Fragment).
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Phytochemistry 31:731-735(1992)
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EMBL, AJ251881; CAB71327.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Calabi F., Cilli V.;
"CBRAZI, a gene rearranged in human leukemia, is a member of multigene family.";
Genomics 52:332-341(1998).
EMBL; AF052211; AAC64700.1;
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01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Heavy metal-responsive transcription factor (Fragment).
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MTGB related protein (Fragment)
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SEQUENCE FROM N.A.

MEDLINE-93222087; PubMed-7682097;

Dong S., Geng J.P., Tong J.H., Wu., et al;

Mang Z.Y., Larsen C.J., Berger R., et al;

Breakpoint clusters of the PML gene in acute promyelocytic leukemia: primary structure of the reciprocal products of the PML-RARA gene in a patient with t(15:17).";

Genes Chromosomes Cancer 6:133-139(1993).
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Leavenworthia.
NCBL_TaxID=70805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1099 MW; A8653693773772C6 CRC64;
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
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01-NOV-1996 (TrEMBLE). 01,
01-DEC-2001 (TrEMBLE). 19,
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Best Local Similarity:
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Salah-Bey K., Doumith M., Michel J.M., Haydock S., Cortes J.,
Leadiay P.F., Raynal M.C.;
"Targetted gene inactivation for the elucidation of deoxysugar
blosynthesis in the erythromycin producer saccharopolyspora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           erythraea.";
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Y14332; CAA74712.1; ...
SEQUENCE FROM N.A.
STRAIN-CV. CR8919/CR15, AND CV. CR8919/CD6;
Liu F., Charlesworth D., Kreitman M.;
Submitted (WAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF054493; AAC19033.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharopolyspora erythraea (Streptomyces erythraeus).
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Pseudonocardineae; Pseudonocardiaceae;
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Last annotation update)
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11 AA; 1208 MW; 5026B3A4BDD87337 CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
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NCBI_TaxID=1836;
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Mihovilovic M., Mai Y., Herbstreith M., Rubboll F., Tarroni P., Clementi F., Roses A.D.;
"Splicing of an anti-sense Alu sequence generates a coding sequence variant for the alpha-3 subunit of a neuronal acetylcholine,
Glycophorin C (Fragment).

Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                               "The association of the glycophorin C exon 3 deletion with ovalocytosis and malaria susceptibility in the Wosera, Papua New
                                                                                                                             Patel S.S., Mehlotra R.K., Kastens W., Mgone C.S., Kazura Jaw.,
Zimmerman P.A.;
                                                                                                                                                                                                                         Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases EMBL; AF342984; AAK01459.1; -.
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1282 MW; 8B0B423A6FC1B2D5 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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EMBL: L18973; AAA86792.1;
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MEDLINE-94071933; PubMed-8250918;
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12 AA; 1361 MW;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Genisteae; Lupinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bublot M., Lomonte P., Lequarre A.-S., Albrecht J.-C., Nicholas J., Fleckenstein B., Pastoret P.-P., Thiry E.; Genetic relationships between bovine herpesvirus 4 and the "Genetic relationships between bovine herpesvirus 5 pstein. Barr virus and herpesviruses Epstein. Barr virus and herpesvirus saimiri."; Virology 190:654-665(1992).

EMBL. M90772; AAA46019.1; -

SEQUENCE 12 AA. 1338 MM; 4B800FF17BCDDDD7 CRC64:
                                                                                                                                                                                                                                                                                                                  STRAIN-CY. PERUS;
POGKOWINSKI J., Grabowska B., Kisiel A., Dlugaszewska B. Nimmagadda G.;
"ENDOAGOB from Lupihus luteus.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF352375; AAK51422.1;
EMBL; AF352372; AAK51419.1;
SEQUENCE 12 AA; 1403 MW; 283958AE7CB326C3 CRC64;
                                                                                                                   Created)
Last sequence update)
Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Herpesvirus saimiri gene 7 homologue (Fragment).
Bovine herpesvirus 4.
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MEDLINE-92391082; PubMed-1325698;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Polyubiquitin homolog (Fragment).
Zea mays (Maize).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PARAIN-CV. INRA 258; TISSUE-LEAF;
MEDLINE-96236829; PubMed-8680303;
MEDLINE-96236829; PubMed-8680303;
MEDLINE-97can L., Frendo P., Nasser W., Genot G., Marivet J., Burkard G.;
"Heavy-metal-responsive genes in maize: identification and comparison of their expression upon various forms of abiotic stress.";
Planta 199:1-8(1996).

EMBL; S82313; AAB47175.1;
                                                                                                                                                                                                                     MEDLINE=92218434; PubMed=1560006; Rato K., Shinohara H., Goto S., Inaguma Y., Morishita R., Asano T.; "Copurification of small heat shock protein with alpha B crystallin from human skeletal muscle."; J. Biol. Chem. 267:7718-7725(1992).
                                                                      01-MAY-2000 (TEMBLTEI. 13, Last sequence update)
01-JUN-2002 (TEMBLTEI. 21, Last annotation update)
Alpha B crystallin fragment 5 (Fragment).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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SEQUENCE 12 AA; 1268 MW; D37BD529CCC1B2CD CRC64;
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                        PRELIMINARY;
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Mismatches:

561 CACCCACCCCCTGGC 57.5

Percent Similarity: Best Local Similarity:

Query Match:

Alignment Scores: Pred. No.:

Indels:

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"Additional organizational features of the murine gamma-glutamyl hydrolase gene. Two remotely situated exons within the complement C3 hydrolase gene. Two remotely situated exons within the complement C3 gene locus encode an alternate 5' end and proximal ORF under the control of a bidirectional promoter."; Gene 268:183-194(2001).

Gene 268:183-194(2001).

Hydrolase:
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Arch. Virol. 146:279-292(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.NCBI_TaxID=10407;
                                                                                                               7EBA4BEA194E2734 CRC64;
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MEDLINE=21213459; PubMed=11315638;
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InterPro; IPR000236; TransactX.
Pfam; PF00739; X; 1.
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Q9E1V4
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  Seprencia
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MEDIINE-98434456; PubMed-9756990;
ESAKI T., ROY K., TAO R., Gallvan J., Sirotnak F.M.;
"Cloning of mouse gamma-glutamyl hydrolase in the form of two cDNA variants with different 5' ends and encoding alternate leader peptide
                                                                                                                                                                                                                                                                                                                                        Bublot M., Lomonte P., Lequarre A.-S., Albrecht J.-C., Nicholas J., Flecknstein B., Pastoret P.-P., Thiry B.; Genetic relationships between bovine herpesvirus 4 and the "Genetic relationships between bovine herpesvirus 4 and the yammaherpesviruses Epstein-Barr virus and herpesvirus salmiri."; Virology 190:654-665(1992).

EMBL: M90772; ARA46019.1; -...
10. 12. 12. 12. 12.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae.
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TremBlrel. 19, Last annotation update)
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Matches:
Conservative:
Mismatches:
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STRAIN-129/SVU; TISSUE-SPLEEN;
MEDLINE-21261955; Pubmed-11368914;
Masumoto N., Esaki T., Sirotnak F.M.;
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01-DEC-2001 (TrEMBLrel. 19, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last anno
                           US-09-824-647-16 (1-2095) x Q69232 (1-12)
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
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Best Local Similarity:
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US-09-824-647-16 (1-2095) x Q9E1U9 (1-13)
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                                                          STRAIN-2F-2;
MEDLINE-21213459; PubMed-11315638;
MEDLINE-21213459; PubMed-11315638;
MEDLINE-21213459; PubMed-11315638;
MEDLINE-21213459; PubMed-11315638;
MEDLINE-21213459; PubMed-11315638;
MEDLINE-21213459; Rim Y., Sohn J., Cho Y.J., Kim Y.;
Medler variation of Hepatitis B virus promoter regions in persistently infected patients.",
Persistently infected patients.",
Arch. Virol. 146:279-292(2001).
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EMBL, AF276521; AAG29988.1; -
InterPro; IPR000236; Transactx.
Hepatitis B virus.
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
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NCBL_raxID=10407;
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EMBL; AF2/6520; AAG29987.1; -.
InterPro; IPR000236; TransactX.
Pfam; PF00739; X; 1.
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                           NCBI_TaxID=10407;
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STRAIN=2F-6;
MEDLINE=21213459; PubMed=11315638;
MEDLINE=21213459; PubMed=11315638;
Ma-Lee Y.M., Lee J., Pyun H., Kim Y., Sohn J., Cho Y.J., Kim Y.;
Sequence variation of Hepatitis B virus promoter regions in persistently infected patients.";
Arch. Virol. 146:279-292(2001).
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MEDLINE-21213459; PubMed-11315638;
MEDLINE-21213459; PubMed-11315638;
MEDLINE-21213459; PubMed-11315638;

Sacuence variation of Hepatitis B virus promoter regions in persistently infected patients.";

Parch. Virol. 146:279-292(2001).
                                                                                               Hepatitis B virus.
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
NCBI_TaxID=10407;
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NCBL_raxID-10407;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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InterPro; IPR000236; TransactX.
Pfam; PF00739; X; 1. 13
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InterPro; IPR000236; TransactX
PFfam; PF00739; X; 1...
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Ha-Lee Y.M., Lee J., Pyun H., Kim Y., Sohn J., Cho Y.J., Kim Y.; "Sequence variation of Hepatitis B virus promoter regions in persistently infected patients."; Arch. Virol. 146:279-222(2001).

EMBL; AF276529; AG29996.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Ha-Lee Y.M., Lee J., Pyun H., Kim Y., Sohn J., Cho Y.J., Kim Y.; Sequence variation of Hepatitis B virus promoter regions in persistently infected patients.";
Arch. Virol. 146:279-292(2001).
EMBU. ARZ16528 AGZ9995.1;
InterPro; IPR00236; Transactx.
Pfam; PF00739; X; 1.
                                                                                                                                                                                                                                                                                                                            Hepatitis B virus.
Viruses; Retroid Viruses; Hepadnaviridae; Orthohepadnavirus.
NCBI_TaxID=10407;
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NCBI_TaxID=10407;
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MEDLINE=21213459; PubMed=11315638;
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MDEL/INS-21213459; PubMed-11315638;
Ha-Lee Y.M., Lee J., Pyun H., Kim Y., Sohn J., Cho Y.J., Kim Y.;
Ha-Lee Y.M., Lee J. Pyun H., Kim Y., Sohn J., Cho Y.J., Kim Y.;
Sequence variation of Hepatitis B virus promoter regions in Sersistently infected patients.";
Arch. Virol 16-279-292(2001).
EMBL: AR27657; AAG29941:--
InterPro; IRR000236; TransactX.
                                                                                                                                                                                                                                                                                                                            Sohn J., Cho Y.J., Kim Y.;
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Ha-Lee Y.M., Lee J., Pyun H., Kim Y., Sohn J., Cho Y.J., Kim "Sequence variation of Hepatitis B virus promoter regions in persistently infected patients.";
Arch. Virol. 146:279-292(2001).
EMBL; AF276525; AAG29992.1; -.
InterPro; IPR000236; TransactX.
Pfam, PF00739; X; 1.
SEQUENCE 13 AA; 1434 MW; 99C40D3FFD0FDEBE CRC64;
                                                                                                                                                                                                           Hepatitis B virus.
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
NCBL_TaxID=10407;
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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InterPro; IPR000236; TransactX.
Pfam; PF00739; X; 1.
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Ha-Lee Y.M., Lee J., Pyun H., Kim Y., Sohn J., Cho Y.J., Kim Y.; "Sequence variation of Hepatitis B virus promoter regions in persistently infected patients."; Arch. Virol. 146.279-292 (2001).

EMBL; AF276532; AAG299991; -. InterPro; IPR000236; TransactX.
STRAIN-4F-4;

MEDLINE-21213459; PubMed-11315638;

MEDLINE-21213459; PubMed-11315638;

MEDLINE-21213459; PubMed-11315638;

"Sequence variation of Hepatitis B virus promoter regions in persistently infected patients.";

persistently infected patients.";

EMBL; AR279531; ARG29981; --
interPro; IPR000236; TransactX.
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NCBL_raxID-10407;
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Ha-Lee Y.M., Lee J., Pyun H., Kim Y., Sohn J., Cho Y.J., Kim Y., Separater and the perfect of the perfect of the persistently infected patients.";

Arch. Virol. ;146:279-292(2001).

BMBL, ARZ16535, AAG30002.1;

InterPro; IPR00236; TransactX.
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01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Homology with C-terminus of other Rhizobium nodB genes.
Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-97002748; PubMed-8850088; Scott D.B., Young C.A., Collins Emerson J.M., Terzaghi E.A., Rockman E.S., Lewis P.E., Pankhurst C.E.; "Novel and complex chromosomal arrangement of Rhizobium lotinodulation genes.";
                                                                                                                                                   Hepatitis B virus.
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
NCBL_TaxID=10407;
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SEQUENCE 13 AA; 1434 MW; 99C40D3FFD0FDEBE CRC64;
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                                                                                 Last sequence update)
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EMBL; L06241; AAB47352.1; -.
SEQUENCE 14 AA; 1600 MW; 90C26EC32C8F34C5
                                      13 AA.
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Matches:
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-MAR-2001 (TrEMBLrel. 16, Last ann
                                                                     Created)
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MEDLINE-21213459; Pubmed-11315638;
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Arch. Virol. 146:279-292(2001).
                                                                                                                                              Ha-Lee Y.M., Lee J., Pyun H., Kim Y., Sohn J., Cho Y.J., Kim "Sequence variation of Hepatitis B virus promoter regions in
                             Hepatitis B virus.
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
NCBI_TaxID=10407;
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Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
NCBL_TaxID=10407;
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                                                                                                               STRAIN=4F-2;
MEDLINE~21213459; PubMed~11315638;
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Arch. Virol. 145:279-292(2001).
MEDI, AF276533, AAG30000.1; -.
InterPro; IPR000236; TransactX.
Pfam; PF00739; X; 1.
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